GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:37:26 ; Search time 5458.54 Seconds
(without alignments)
10242.778 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactcacggtcaagct.....ggaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1048.4	87.7	1050	10	AY403218	AY403218 Homo sapi
	2	931.6	78.0	1045	10	AY403219	AY403219 Pan trogl
	3	841	70.4	884	6	CA488012	CA488012 AGENCOURT
	4	806	67.4	1211	4	AK010437	AK010437 Mus muscu
	5	765.2	64.0	1050	10	AY403220	AY403220 Mus muscu
c	6	718.4	60.1	720	6	CA446381	CA446381 UI-H-ED1-
	7	692.8	58.0	881	2	BG565247	BG565247 602582917
	8	683.2	57.2	961	2	BG762026	BG762026 602718984
	9	672.4	56.3	827	8	CV983083	CV983083 UMC-bmix_
	10	672	56.2	710	2	BE875216	BE875216 601488516
	11	663	55.5	697	8	DN997716	DN997716 TC115356
	12	657.6	55.0	773	5	BU602279	BU602279 AGENCOURT
	13	656.2	54.9	742	8	CX757709	CX757709 AGENCOURT
	14	655	54.8	783	3	BI552907	BI552907 603197827
	15	654.6	54.8	825	8	CX753134	CX753134 AGENCOURT
	16	642.4	53.8	796	2	BG182296	BG182296 RST1161 A
c	17	640.8	53.6	788	7	CN153902	CN153902 941069 MA
c	18	640.4	53.6	661	3	BM995067	BM995067 UI-H-ED0-
	19	634.2	53.1	799	5	BU930271	BU930271 AGENCOURT
c	20	600	50.2	600	1	AI686139	AI686139 tt92e11.x
	21	598	50.0	609	6	CD677954	CD677954 ho24h02.y
	22	597.8	50.0	920	2	BE881257	BE881257 601492338
	23	596.8	49.9	1003	3	BI551229	BI551229 603194629
	24	589	49.3	1071	3	BM920324	BM920324 AGENCOURT
c	25	588	49.2	705	6	CB424830	CB424830 599432 MA
	26	587	49.1	684	2	BE439545	BE439545 HTM1-183F
	27	586.2	49.1	609	5	BX103101	BX103101 BX103101
c	28	577.8	48.4	584	3	BM675259	BM675259 UI-E-EJ0-
	29	576.2	48.2	636	6	CD690450	CD690450 EST6973 h
	30	573.4	48.0	581	3	BM714075	BM714075 UI-E-EJ0-
	31	559.4	46.8	891	2	BF965211	BF965211 602268114
c	32	554.4	46.4	581	2	BG577403	BG577403 N112 SSH-
	33	553.8	46.3	773	2	BG104394	BG104394 602311010
	34	550.2	46.0	779	5	BU929991	BU929991 AGENCOURT
	35	534.6	44.7	661	5	BX506262	BX506262 DKFZp686E
	36	521.6	43.6	600	3	BI360480	BI360480 387409 MA
c	37	504.8	42.2	759	6	CA509933	CA509933 UI-R-FS0-
	38	499.6	41.8	705	5	BY755449	BY755449 BY755449
c	39	497	41.6	497	1	AI167942	AI167942 oo09b06.x
	40	494	41.3	1007	6	CF596595	CF596595 AGENCOURT
c	41	484.2	40.5	729	3	BQ211210	BQ211210 UI-R-DY1-
	42	476.2	39.8	566	6	CB143042	CB143042 K-EST0196
c	43	475.6	39.8	654	7	CO594327	CO594327 DG2-93n7
c	44	474.4	39.7	696	3	BQ205543	BQ205543 UI-R-EP0-
	45	472.6	39.5	1020	3	BM811413	BM811413 AGENCOURT

ALIGNMENTS

RESULT 1
AY403218
LOCUS AY403218 1050 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens STEAP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY403218
VERSION AY403218.1 GI:39759201
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1050)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1050)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .1050
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>1050
/gene="STEAP"
/locus_tag="HCM1484"
ORIGIN

Query Match 87.7%; Score 1048.4; DB 10; Length 1050;
Best Local Similarity 99.9%; Pred. No. 2.1e-232;
Matches 1049; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy         36 TGGCTGAAGCCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAA 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGGCTGAAGCCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAA 60

Qy         96 GAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAAG 155
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAAG 120

Qy        156 GACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCC 215
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        121 GACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCAGCAAACAGCC 180

Qy        216 CATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAG 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAG 240

Qy        276 TGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTT 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTT 300

Qy        336 CTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCA 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCA 360

Qy        396 ATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTAC 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTAC 420

Qy        456 CTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTT 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTT 480

Qy        516 CCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTT 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTT 540

Qy        576 TTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATAC 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATAC 600

Qy        636 AAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAG 695
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAG 660

Qy        696 CATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTG 755
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTG 720

Qy        756 GCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTT 815
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTT 780

Qy        816 CACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTG 875
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTG 840

Qy        876 ATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAACT 935
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 ATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAACT 900

Qy        936 TTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTG 995
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTG 960

Qy        996 CCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATT 1055
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATT 1020

Qy       1056 AACAAAACTGAGATATGTTCCCAGTTGTAG 1085
              |||||||||||||||||||||||||||||
Db       1021 AACAAAACTGAGATATGTTCCCAGTTGTAG 1050
```

```
RESULT 2
AY403219
LOCUS       AY403219               1045 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Pan troglodytes STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403219
VERSION     AY403219.1  GI:39759202
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1045
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>1045
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN
```

```
  Query Match           78.0%;  Score 931.6;  DB 10;  Length 1045;
  Best Local Similarity  89.4%;  Pred. No. 2.7e-205;
  Matches  934;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy         41 GAAGCCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGA 100
              ||||||||||||||| ||||||||||||||||      ||||||||||||||||||||
Db          1 GAAGCCATACTATTNTATAGAATTAATGGAAANNNNNNAAGACATCACAAACCAAGAAGA 60

Qy        101 ACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACAC 160
              | ||||||                                          ||||||||||
Db         61 AATTTGGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNCATAAGGACAC 120

Qy        161 GGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGC 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGC 180

Qy        221 TGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCA 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCA 240

Qy        281 CTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAG 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAG 300

Qy        341 GGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCT 400
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCT 360

Qy        401 GGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCC 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        361 GGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCC 420

Qy        461 AGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACA 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACA 480

Qy        521 TTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGC 580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGC 540

Qy        581 TGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTT 640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTT 600

Qy        641 GCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGA 700
              |||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        601 GCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGANNNTGCCTGGATTGAGCATGA 660

Qy        701 TGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCT 760
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCT 720

Qy        761 GTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTA 820
              ||||||||||||
Db        721 GTTGGCTGTGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 780

Qy        821 TATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTT 880
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 NNNNNNAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTT 840

Qy        881 TGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTAT 940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTAT 900

Qy        941 GATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATG 1000
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATG 960

Qy       1001 CTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAA 1060
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAA 1020

Qy       1061 AACTGAGATATGTTCCCAGTTGTAG 1085
              |||||||||||| ||||||||||||
Db       1021 AACTGAGATATCTTCCCAGTTGTAG 1045
```

```
RESULT 3
CA488012
LOCUS       CA488012                 884 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10807821 MAPcL Homo sapiens cDNA clone IMAGE:6719746 5',
            mRNA sequence.
ACCESSION   CA488012
VERSION     CA488012.1  GI:24948800
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14278  row: c  column: 10
            High quality sequence stop: 758.
FEATURES             Location/Qualifiers
     source          1. .884
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6719746"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification:  26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN
```

Query Match 70.4%; Score 841; DB 6; Length 884;
Best Local Similarity 99.4%; Pred. No. 2.9e-184;
Matches 844; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 76

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 136

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 196

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 256

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 316

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        317 CTATTATAGCATCTCTGACTTTTCTCTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 376

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 436

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 496

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 556

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 616

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 676

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        677 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 736
```

```
Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        737 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 796

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        797 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 856

Qy        841 TTGTTTCCC 849
                |  || ||
Db        857 ATTGTTTCC 865
```

RESULT 4
AK010437
LOCUS AK010437 1211 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410007B19 product:six transmembrane epithelial antigen of the prostate, full insert sequence.
ACCESSION AK010437
VERSION AK010437.1 GI:12845880
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 1211)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

FEATURES Location/Qualifiers
source 1. .1211
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:2410007B19"
/db_xref="taxon:10090"
/clone="2410007B19"
/cell_type="ES cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
CDS 98. .1117
/note="unnamed protein product; putative six transmembrane epithelial antigen of the prostate (MGD|MGI:1917608, GB|AK010437, evidence: BLASTN, 100%, match=1211)"
/codon_start=1
/protein_id="BAB26938.1"
/db_xref="GI:12845881"
/translation="MEISDDVTNPEQLWKMKPKGNLEDDSYSTKDSGETSMLKRPGLS HLQHAVHVDAFDCPSELQHTQEFFPNWRLPVKVAAIISSLTFLYTLLREIIYPLVTSR EQYFYKIPILVINKVLPMVAITLLALVYLPGELAAVVQLRNGTKYKKFPPWLDRWMLA KKQFGLLSFFFAVLHAVYSLSYPMRRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRMEI YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNK WVDVSQFVWYMPPTFMIAVFLPTLVLICKIALCLPCLRKKILKIRCGWEDVSKINRTE MASRL"
polyA_signal 1186. .1191
/note="putative"
polyA_site 1211
/note="putative"

ORIGIN

Query Match 67.4%; Score 806; DB 4; Length 1211;
Best Local Similarity 81.0%; Pred. No. 4e-176;
Matches 952; Conservative 0; Mismatches 220; Indels 4; Gaps 1;

```
Qy          3 GAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAGAA 62
              | | ||| | ||| |       ||  ||  ||||||||||||| ||||||||||||| |
Db         35 GCGCCTCGCCGTCGGGTCCCACGGAGAAGCCGGTGGCTGAAGCCGTACTATTTTATAGCA 94

Qy         63 TTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG 122
               | ||||| | |||  | ||  | ||||||| |||| ||||||||||||||||||| | |
Db         95 GTCATGGAGATCAGTGACGATGTTACAAACCCAGAACAACTTTGGAAAATGAAGCCAAAG 154

Qy        123 AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAA 182
              ||||  | ||||| |||  ||| | |  ||||||| |||||||||| ||||||||  |||
Db        155 GGAAACCTGGAAGATGACAGTTACTCGACTAAGGACTCGGGAGAGACGAGCATGCTGAAA 214

Qy        183 AGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA 242
```

```
Db        215 AGACCGGGGCTCTCGCACTTGCAGCACGCGGTCCACGTCGATGCCTTTGACTGCCCCTCC 274

Qy        243 GAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCT 302

Db        275 GAGCTTCAGCACACGCAGGAATTCTTTCCAAACTGGCGCTTGCCAGTGAAAGTCGCTGCC 334

Qy        303 ATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCA 362

Db        335 ATCATATCATCCCTGACTTTCCTGTACACACTTCTGAGGGAAATCATCTACCCGTTAGTA 394

Qy        363 ACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCA 422

Db        395 ACTTCCCGTGAACAATATTTTTATAAAATTCCAATCCTGGTTATTAACAAAGTCTTGCCA 454

Qy        423 ATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTC 482

Db        455 ATGGTCGCCATTACCCTCTTGGCACTGGTCTATTTGCCAGGAGAGTTAGCGGCAGTTGTA 514

Qy        483 CAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTA 542

Db        515 CAGCTTCGCAATGGAACCAAGTACAAGAAGTTCCCACCCTGGTTAGATAGATGGATGCTG 574

Qy        543 ACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGT 602

Db        575 GCCAAGAAGCAGTTTGGTCTCCTCAGCTTCTTTTTTGCTGTGCTGCACGCTGTTTACAGT 634

Qy        603 CTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAG 662

Db        635 CTCTCATACCCAATGAGGAGATCCTACAGATACAAGCTACTCAACTGGGCTTACAAACAG 694

Qy        663 GTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTAT 722

Db        695 GTTCAACAAAACAAAGAGGATGCCTGGGTAGAGCATGATGTCTGGAGAATGGAGATTTAT 754

Qy        723 GTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCA 782

Db        755 GTGTCCCTGGGGATTGTGGGGCTGGCCATCTTGGCTCTCTTGGCTGTGACATCTATTCCA 814

Qy        783 TCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATT 842

Db        815 TCTGTGAGCGACTCTTTAACCTGGAGAGAATTTCACTATATTCAGAGCAAACTAGGAATT 874

Qy        843 GTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGAT 902

Db        875 GTCTCTCTTCTTCTGGGCACAGTACACGCTTTGGTTTTTGCCTGGAATAAATGGGTAGAT 934

Qy        903 ATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATT 962

Db        935 GTCAGTCAATTTGTATGGTACATGCCTCCGACTTTTATGATAGCTGTTTTCCTTCCAACT 994

Qy        963 GTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAG 1022

Db        995 CTTGTCCTGATATGTAAAATCGCCCTGTGCCTGCCCTGTCTGAGGAAGAAGATACTGAAG 1054

Qy       1023 ATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

Db       1055 ATTAGATGTGGTTGGGAAGATGTCAGCAAAATTAACAGGACTGAGATGGCCTCCAGGTTG 1114

Qy       1083 TAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTC 1142

Db       1115 TAGAACTACTGTTTGCACATATTTGCTTGTTAT----TGATGTCCTATCATAAGCATTTC 1170

Qy       1143 AAGTTTGTATTTGTTAATAAAATGATTATTCAAGGA 1178

Db       1171 AAATTTGTGTTTGTTAATAAAATGAATACTTTGGGA 1206


RESULT 5
AY403220
LOCUS       AY403220                1050 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403220
VERSION     AY403220.1  GI:39759203
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1050
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>1050
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

  Query Match             64.0%;  Score 765.2;  DB 10;  Length 1050;
  Best Local Similarity   83.0%;  Pred. No. 1.1e-166;
  Matches  872;  Conservative    0;  Mismatches  178;  Indels    0;  Gaps    0;

Qy         36 TGGCTGAAGCCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAA 95

Db          1 TGGCTGAAGCCGTACTATTTTATAGCAGTCATGGAGATCAGTGACGATGTTACAAACCCA 60

Qy         96 GAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAAG 155

Db         61 GAACAACTTTGGAAAATGAAGCCAAAGGGAAACCTGGAAGATGACAGTTACTCGACTAAG 120

Qy        156 GACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCC 215

Db        121 GACTCGGGAGAGACGAGCATGCTGAAAAGACCGGGGCTCTCGCACTTGCAGCACGCGGTC 180

Qy        216 CATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAG 275

Db        181 CACGTCGATGCCTTTGACTGCCCCTCCGAGCTTCAGCACACGCAGGAATTCTTTCCAAAC 240

Qy        276 TGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTT 335

Db        241 TGGCGCTTGCCAGTGAAAGTCGCTGCCATCATATCATCCCTGACTTTCCTGTACACACTT 300

Qy        336 CTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCA 395

Db        301 CTGAGGGAAATCATCTACCCGTTAGTAACTTCCCGTGAACAATATTTTTATAAAATTCCA 360

Qy        396 ATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTAC 455

Db        361 ATCCTGGTTATTAACAAAGTCTTGCCAATGGTCGCCATTACCCTCTTGGCACTGGTCTAT 420

Qy        456 CTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTT 515

Db        421 TTGCCAGGAGAGTTAGCGGCAGTTGTACAGCTTCGCAATGGAACCAAGTACAAGAAGTTC 480
```

```
Qy        516 CCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTT 575
              ||||  ||||| ||||  |||||| |  | || ||||||||||| || ||||| ||||||
Db        481 CCACCCTGGTTAGATAGATGGATGCTGGCCAGGAAGCAGTTTGGTCTCCTCAGCTTCTTT 540

Qy        576 TTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATAC 635
              |||||||| ||||| ||  |||| ||||| || ||||||||||||| ||||||||||||||
Db        541 TTTGCTGTGCTGCACGCTGTTTACAGTCTCTCATACCCAATGAGGAGATCCTACAGATAC 600

Qy        636 AAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAG 695
              ||| | || |||||||| ||  ||||||| |||||||| ||||| |||||||||  | |||
Db        601 AAGCTACTCAACTGGGCTTACAAACAGGTTCAACAAAACAAAGAGGATGCCTGGGTAGAG 660

Qy        696 CATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTG 755
              |||||||| ||||||||||||||||||||||| ||||| ||||||||  |||| ||  ||
Db        661 CATGATGTCTGGAGAATGGAGATTTATGTGTCCCTGGGGATTGTGGGGCTGGCCATCTTG 720

Qy        756 GCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTT 815
              ||||| ||||||||||||||||||||||||||||| |||||||| || ||||||||||||
Db        721 GCTCTCTTGGCTGTGACATCTATTCCATCTGTGAGCGACTCTTTAACCTGGAGAGAATTT 780

Qy        816 CACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTG 875
              |||||||||||||||| |||||||||| || ||||| ||||||||| ||||||| |||
Db        781 CACTATATTCAGAGCAAACTAGGAATTGTCTCTCTTCTTCTGGGCACAGTACACGCTTTG 840

Qy        876 ATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAACT 935
              |||||||||||||||| ||| ||||| | |  |||||||||||||| |  ||||| |||
Db        841 GTTTTTGCCTGGAATAAATGGGTAGATGTCAGTCAATTTGTATGGTACATGCCTCCGACT 900

Qy        936 TTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTG 995
              |||||||||||||||||||||||| | |||||||||||| |||||  |   || | ||||
Db        901 TTTATGATAGCTGTTTTCCTTCCAACTCTTGTCCTGATATGTAAAATCGCCCTGTGCCTG 960

Qy        996 CCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATT 1055
              || ||  |||||||||||||||||||||||||  |||||||||||| |||| |||||||
Db        961 CCCTGTCTGAGGAAGAAGATACTGAAGATTAGATGTGGTTGGGAAGATGTCAGCAAAATT 1020

Qy       1056 AACAAAACTGAGATATGTTCCCAGTTGTAG 1085
              ||||  ||||||||    |||  |||||||
Db       1021 AACAGGACTGAGATGGCCTCCAGGTTGTAG 1050
```

RESULT 6
CA446381/c

```
LOCUS       CA446381                720 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-ED1-axr-o-23-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
            UI-H-ED1-axr-o-23-0-UI 3', mRNA sequence.
ACCESSION   CA446381
VERSION     CA446381.1  GI:24810801
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-ED1-axr-o-23-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_ED1"
                     /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
                     containing the following tissue(s): Chondrosarcoma cell
                     line CS5. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GCTCAAGGCT.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-ED1
                     TAG_SEQ=CGTCAAGGCT"
ORIGIN
```

Query Match 60.1%; Score 718.4; DB 6; Length 720;
Best Local Similarity 99.9%; Pred. No. 8e-156;
Matches 719; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        476 AATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTG 535
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 AATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTG 661

Qy        536 GATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAAT 595
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        660 GATGTTAACAAGAAAGCAGTCTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAAT 601

Qy        596 TTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATA 655
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 TTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATA 541

Qy        656 TCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGA 715
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 TCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGA 481

Qy        716 GATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATC 775
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATC 421

Qy        776 TATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCT 835
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCT 361

Qy        836 AGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTG 895
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTG 301

Qy        896 GATAGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCT 955
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GATAGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCT 241

Qy        956 TCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAT 1015
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAT 181

Qy       1016 ACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTC 1075
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 ACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTC 121

Qy       1076 CCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCA 1135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 CCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCA 61
```

```
Qy       1136 ACATTTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 ACATTTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1
```

RESULT 7
BG565247
LOCUS BG565247 881 bp mRNA linear EST 10-APR-2001
DEFINITION 602582917F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710436 5', mRNA sequence.
ACCESSION BG565247
VERSION BG565247.1 GI:13572900
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 881)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1549 row: b column: 05
High quality sequence stop: 704.
FEATURES Location/Qualifiers
source 1. .881
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4710436"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_76"
/note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.85 kb (range 1.0-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 58.0%; Score 692.8; DB 2; Length 881;
Best Local Similarity 92.0%; Pred. No. 7.2e-150;
Matches 786; Conservative 0; Mismatches 62; Indels 6; Gaps 5;

```
Qy        251 GCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGC 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGC 60

Qy        311 ATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCA 370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCA 120

Qy        371 TCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTC 430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTC 180

Qy        431 CATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCA 490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCA 240

Qy        491 TAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAA 550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TAATGGAACCAAGTATAAGAAGTTTCCACAGTGGTTGGATAAGTGGATGTTAACAAGAAA 300

Qy        551 GCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTA 610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTA 360

Qy        611 CCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACA 670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACA 420

Qy        671 AAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT 730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAATAAAGAAGATGCCTGGATTGAGCATGATGTCTGGAGAATGGAGATTTATGTGTCTCT 480

Qy        731 GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAG 790
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGAATTGTGGGATTGG-AATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAG 539

Qy        791 TGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCT 850
              |||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||||
Db        540 TGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGGAAGCTAGGAATAGTTTCCCT 599

Qy        851 TCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGG--ATAGATATAAAA 908
              |||||||||||||||||||||||||||||||| ||||||||||||||        |||||
Db        600 TCTACTGGGCACAATACACGCATTGATTTTGGCCTGGAATAAGTGGGATAGATCATAAAC 659

Qy        909 CAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTC 968
              | ||||||||||||||||||||||||||||||||||||||| | | | | |       |
Db        660 ACAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAATTGTAGTCC 719

Qy        969 CTGATATTT-AAAAGCATACTATT-CCTGCCATGCTTGAGGAAGAAGATACT-GAAGATT 1025
              ||||||||| ||| |||||||||| | |||||||||||| | |||||||||| || ||||
Db        720 CTGATATTTCAAACGCATACTATTACTTGCCATGCTTGAAGCAGAAGATACTGGACGATT 779

Qy       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAG 1085
              |||| ||||||||||||     |   ||      |||||||||| ||| |   |  | |
Db        780 AGACTTGGTTGGGAAGAACGTCCACCAAAATCAAAAACTGAGATTTGTCCAGTGGAGAAT 839

Qy       1086 AATTACTGTTTACA 1099
              |  |  |   |||
Db        840 ACCTGGTTACCACA 853

RESULT 8
BG762026
LOCUS BG762026 961 bp mRNA linear EST 15-MAY-2001
DEFINITION 602718984F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4858820 5', mRNA sequence.
ACCESSION BG762026
VERSION BG762026.1 GI:14072679
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 961)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1713 row: h column: 21
High quality sequence stop: 750.
```

```
FEATURES             Location/Qualifiers
     source          1. .961
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4858820"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_49"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using  ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library. |"
ORIGIN

  Query Match             57.2%;  Score 683.2;  DB 2;  Length 961;
  Best Local Similarity   93.2%;  Pred. No. 1.2e-147;
  Matches  772;  Conservative    0;  Mismatches   43;  Indels   13;  Gaps    5;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              | |||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||
Db         57 CTGAGACTCACGGTCAAGCTACGGCGAGGAGTGGGTGGCTGAAGCCATACTATTTTATAG 116

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        117 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAATTTGGAAAATGAAGCCTA 176

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        177 GGAGAAATTTAGAAGACAACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 236

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        237 AAAGACCTGTGCTTTTGCATTTGCAGCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 296

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 CAGAACTTCAGCACGCACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 356

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 CTGTTATGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 416

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 476

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        477 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTACCAGGTGTGATAGCAGCAATTG 536

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TCCAAGTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 596

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              |||||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db        597 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTT-GGTTTTGCTGTACTGCATGCAATTTATA 655

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 CTCTGTCTTACGCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 715

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAAT--GGAGAT 718
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||  |    |
Db        716 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTCGGAGAATGCGCCACT 775

Qy        719 TTATGTGTCTCTGGGAATTGTGGGATTGGC-------AATACTGGCTCTGTTGGC--TGT 769
              | ||||||| | ||| | | || |   | |         |    ||||||||||||    |
Db        776 TCATGTGTCCCCGGGGACTTTGTGGCGGACGGGGCAACACTTGGGCTCTGTTGGCCTGTT 835

Qy        770 GACATCTATTCCATCTGTGA-GTGACTCTTTGACATGGAGAGAATTTC 816
              |||||||||||||||||||| ||||| ||||||| ||| ||||||| |
Db        836 GACATCTATTCCATCTGTGACGTGACCCTTTGACCTGGCGAGAATTCC 883


RESULT 9
CV983083
LOCUS       CV983083                827 bp    mRNA    linear   EST 30-NOV-2004
DEFINITION  UMC-bmix_0B02-007-e08 Conceptus-Corpus Luteum (mixed) bmix Bos
            taurus cDNA 3', mRNA sequence.
ACCESSION   CV983083
VERSION     CV983083.1  GI:56143804
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 827)
  AUTHORS   Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
            Roberts,R.M., Smith,M.F. and Youngquist,R.S.
  TITLE     USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
            Reproduction
  JOURNAL   Unpublished (2002)
COMMENT     Contact: DNA Core Facility (Bovine Project)
            Animal Science - RS Prather
            University of Missouri-Columbia
            M616 Medical Sciences Bldg., Columbia, MO 65212, USA
            Tel: (573)882-0428
            Fax: (573)884-5552
            Email: bovine@rnet.missouri.edu
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .827
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /dev_stage="Conceptus-Corpus Luteum(mixed)"
                     /clone_lib="bmix"
                     /note="Vector: pSport1; Funding: The production of ESTs
                     submitted in this project was funded by USDA Grant
                     MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
                     Reproduction' to RS Prather(Primary Investigator), E
                     Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
                     Smith and RS Youngquist. Genetic Source: Heifers for the
                     project were purchased from Circle A Ranch, Iberia, MO
                     (http://www.circlearanch.com/home.html). These heifers,
                     while not registered have known Angus pedigrees going back
                     at least 4 generations. Samples collected: The samples
                     consisted of the following: germinal vesicle-stage
                     oocytes; in vitro derived embryos (2-cell, morula,
                     blastocyst and nuclear transfer blastocyst); in vivo
                     blastocysts and conceptuses (days 8, 14, 16 and 18);
                     corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
                     follicles (days 0, non-recruited, recruited, early
                     selected and preovulatory); oviduct (days 0, 3 and 5);
                     endometrium (days 5, 8, 14, 16, 18 and 35); and
                     placenta/embryo from day 35 conceptuses. Expanded
                     descriptions of how the tissues were collected can be
                     found at the following URL:
                     http://genome.rnet.missouri.edu/Bovine/Methods.html.
                     Library construction (Standard Protocol): All procedures
                     have been described in detail elsewhere (Soares et al.,
                     1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
                     cellular RNA from each sample was isolated by using
                     STAT-60 reagent (Tel-Test, Friendswood, TX) and the
                     poly(A)+ RNA was obtained by two rounds of purification
                     with the Oligotex mRNA isolation kit (Qiagen) according to
                     the manufacturer's instructions. The libraries were
                     constructed essentially as described by the manufacturer's
```

instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of poly(A)+ RNA was annealed at c37 degrees with 10mcg of NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18)' and reverse transcribed at c37 degrees with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier (http://genome.uiowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@rnet.missouri.edu. Citations: Bonaldo MF, Lennon G, Soares MB,. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_TISSUE=Conceptus-Corpus Luteum (mixed)
TAG_SEQ=Not found"

ORIGIN

```
  Query Match             56.3%;  Score 672.4;  DB 8;  Length 827;
  Best Local Similarity   89.3%;  Pred. No. 3.9e-145;
  Matches  735;  Conservative    0;  Mismatches   87;  Indels    1;  Gaps    1;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              |||  ||| || |||| |  | | | |  || ||||||||||||||||||||||||||||
Db          5 CCGCAACTTACCGTCAGGTCACGACAAGAAGCGGGTGGCTGAAGCCATACTATTTTATAG 64

Qy         61 AATT-AATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCT 119
              |||| |||||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db         65 AATTAAATGGAGAGCAGACAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCT 124

Qy        120 AGGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTA 179
              ||||||||| |||||||||| ||||||||| |||| ||| | | ||||| | |||||||
Db        125 AGGAGAAATCTAGAAGAAGATGATTATTTGAATAAAGACTCAGAAGAGATCGGCATGCTG 184

Qy        180 AAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCT 239
              ||||||| |||||||||||| |||||||||||| |||||  |||||||||||| |||||

Db        185 AAAAGACATGTGCTTTTGCACTTGCACCAAACAACCCATTTTGATGAATTTGATTGCCCC 244

Qy        240 TCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCT 299
              ||||  |||||||| | |||| |||||||||| |||||| ||||||||||||||||||
Db        245 CCAGAGCTTCAGCAAAAACAGAAACTCTTTCCAAAGTGGCGCTTGCCAATTAAAATAGCC 304

Qy        300 GCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTA 359
              |||||| || |||||||||||||||| |||||||| |||||||| ||||||||||||
Db        305 GCTATTGTATCATCTCTGACTTTTCTCTACACTCTTGTGAGGGAAATAATTCACCCTTTT 364

Qy        360 GCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTG 419
              |  |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        365 GTGACTTCCCATCAACAGTATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTG 424

Qy        420 CCAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATT 479
              |||||||||||||||| |||||||| |||||||  |||||||||||||||||||| ||
Db        425 CCAATGGTTTCCATCACCCTCTTGGCACTGGTTTATTTGCCAGGTGTGATAGCAGCAGTT 484

Qy        480 GTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATG 539
              || || ||||||||||||| |||||||||| |||| || |||||||||| |||||||
Db        485 GTGCAGCTTCATAATGGAACTAAGTATAAGAAATTTCCGCACTGGTTGGATAGGTGGATG 544

Qy        540 TTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTAT 599
              |||||||||||||||||| |||||||||||||||||||||||| ||||||||||
Db        545 GTAACAAGAAAGCAGTTTGGTCTTCTCAGTTTCTTTTTTGCTGTACTACATGCAATTTAC 604

Qy        600 AGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAA 659
              ||| | || || || |||||||||||||||||| | |||||| ||||||||||||||||
Db        605 AGTTTATCCTATCCGATGAGGCGATCCTACAGATATAGGTTGCTGAACTGGGCATATCAA 664

Qy        660 CAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATT 719
              |||||||||||||||| ||| |||||||||||| |||||||||||||||||||| |||
Db        665 CAGGTCCAACAAAATAACGAANATGCCTGGATTGAACATGATGTTTGGAGAATGGAAATT 724

Qy        720 TATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATT 779
              ||||| || |||||||| |||| | | |||||||| ||||| ||||||||||||||||||
Db        725 TATGTATCACTGGGAATCGTGGCACTTGCAATACTAGCTCTATTGGCTGTGACATCTATT 784

Qy        780 CCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATA 822
              |||||||||||||| ||| |||||||||||||||||||||||
Db        785 CCATCTGTGAGTGATTCTCTGACATGGAGAGAATTTCACTATA 827
```

RESULT 10
BE875216

```
LOCUS       BE875216                710 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601488516F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890930 5',
            mRNA sequence.
ACCESSION   BE875216
VERSION     BE875216.1  GI:10323992
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9674  row: p  column: 03
            High quality sequence stop: 701.
FEATURES             Location/Qualifiers
     source          1. .710
```

```
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3890930"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             56.2%;  Score 672;  DB 2;  Length 710;
  Best Local Similarity   99.0%;  Pred. No. 4.7e-145;
  Matches  697;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;

Qy         45 CCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTT 104
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db          1 CCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAC-T 59

Qy        105 TGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGA 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGA 119

Qy        165 GAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGAT 224
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        120 GAGACCAGCATGCTAAAGAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGAT 179

Qy        225 GAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTG 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTG 239

Qy        285 CCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAA 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 CCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAA 299

Qy        345 GTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTC 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTC 359

Qy        405 ATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGT 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGT 419

Qy        465 GTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGG 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 GTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGG 479

Qy        525 TTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTA 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 TTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTA 539

Qy        585 CTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTA 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTA 599

Qy        645 AACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTT 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 AACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTT 659

Qy        705 TGGAGAATGG-AGATTTATGTGTCTCTGGGAATTGTGGGATTGG 747
              |||||||||| |||||||||||||||||||| |||||  | |
Db        660 TGGAGAATGGCAGATTTATGTGTCTCTGGGAATCGTGGGGATTG 703


RESULT 11
DN997716
LOCUS       DN997716                 697 bp    mRNA    linear   EST 17-MAY-2005
DEFINITION  TC115356 Human breast cancer tissue, large insert, pCMV expression
            library Homo sapiens cDNA clone TC115356 5' similar to Homo sapiens
            six transmembrane epithelial antigen of the prostate 1 (STEAP1),
            mRNA sequence.
ACCESSION   DN997716
VERSION     DN997716.1  GI:66257543
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L.,
            Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M.,
            Zhang,X., Jay,G. and He,W.
  TITLE     High-throughput cloning of full-length human cDNAs directly from
            cDNA libraries optimized for large and rare transcripts
  JOURNAL   Unpublished (2005)
COMMENT     Contact: Kovacs, KF
            High Throughput cDNA Cloning
            OriGene Technologies, Inc. ( www.origene.com )
            6 Taft Court, Suite 100, Rockville, MD 20850, USA
            Tel: 301 340 3188
            Fax: 301 340 8606
            Email: cDNA@origene.com
            This EST submission is part of an on-going human full-length
            cloning project at OriGene Technologies, Inc.
            Please contact OriGene for access.
            OriGene Technologies, Inc.
            6 Taft Ct. Suite 100
            Rockville, MD 20850
            Tel: (301) 340-3188
            http://www.origene.com
            Seq primer: pCMV6 5prime forward vector primer, OriGene
            Technologies Inc.
FEATURES             Location/Qualifiers
     source          1. .697
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="TC115356"
                     /tissue_type="Breast cancer"
                     /clone_lib="Human breast cancer tissue, large insert, pCMV
                     expression library"
                     /note="Organ: Mammary gland (cancer tissue); Vector:
                     pCMV6-XL5; Site_1: EcoR1; Site_2: Xho1/Sal1 compatible end
                     ligatio; Oligo-dT primed reverse transcription optimized
                     for large and GC rich mRNA transcripts, cDNA size
                     selection, optimized ligation for large inserts into
                     mammalian expression vector, random clones selected for
                     end sequence verification of full-length genes"
ORIGIN

  Query Match             55.5%;  Score 663;  DB 8;  Length 697;
  Best Local Similarity   100.0%;  Pred. No. 5.8e-143;
  Matches  663;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 94

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 154

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 214

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 274

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 334
```

```
Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 394

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 454

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 514

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 574

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 634

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 694

Qy        661 AGG 663
              |||
Db        695 AGG 697
```

RESULT 12
BU602279
```
LOCUS       BU602279                 773 bp    mRNA    linear   EST 20-SEP-2002
DEFINITION  AGENCOURT_10016846 NIH_MGC_142 Homo sapiens cDNA clone
            IMAGE:6496341 5', mRNA sequence.
ACCESSION   BU602279
VERSION     BU602279.1  GI:23254038
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: NCI
             cDNA Library Preparation: Michael Brownstein Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2675  row: j  column: 22
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
     source          1. .773
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6496341"
                     /tissue_type="mixed (pool of 40 RNAs)"
                     /lab_host="DH10B (T1-phage-resistant)"
                     /clone_lib="NIH_MGC_142"
                     /note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc);
                     Site_2: SfiI (ggccgcctcggcc); Double-stranded cDNA was
                     prepared from a pool of 40 cell line polyA+ RNAs (bladder
                     - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
                     4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
                     kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
                     ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
                     gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
                     used in cloning as follows:
                     5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length
                     enriched library was constructed using the Clontech
                     Creator SMART kit and size-selected to contain the >0.5 kb
                     size fraction (other fractions present in NIH_MGC_141).
                     Library created in the laboratory of M. Brownstein (NIMH,
                     NIH). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             55.0%;  Score 657.6;  DB 5;  Length 773;
  Best Local Similarity   99.1%;  Pred. No. 1e-141;
  Matches  682;  Conservative    0;  Mismatches    4;  Indels    2;  Gaps    2;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 139

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 199

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        200 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 259

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        260 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 319

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        320 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 379

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        380 CTATTATAGCATCTCTGACTTTTCTCTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 439

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        440 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 499

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        500 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 559

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        560 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 619

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        620 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 679

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACT-GGGCATATCAA 659
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        680 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGGCATATCAA 739

Qy        660 CA-GGTCCAACAAAATAAAGAAGATGCC 686
              || ||||| || |||| |||||||||||
Db        740 CAGGGTCCCACCAAATTAAGAAGATGCC 767
```

RESULT 13
CX757709
```
LOCUS       CX757709                 742 bp    mRNA    linear   EST 24-JAN-2005
DEFINITION  AGENCOURT_41384224 NIH_MGC_278 Homo sapiens cDNA clone
            IMAGE:7772991 3', mRNA sequence.
ACCESSION   CX757709
VERSION     CX757709.1  GI:58054365
KEYWORDS    EST.
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Meri Firpo
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15916  row: h  column: 13
            High quality sequence start: 6
            High quality sequence stop: 726.
FEATURES             Location/Qualifiers
     source          1. .742
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7772991"
                     /tissue_type="pluripotent cell line derived from
                     blastocyst inner cell mass"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_278"
                     /note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
                     EcoRV; Site_2: NotI; RNA obtained from pluripotent cell
                     line derived from blastocyst inner cell mass (cell line
                     HSF-1.14, NIH Registry designation UC01. Positive for OCT4
                     expression by rtPCR, positive for SSEA-3, SSEA-4,
                     Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
                     SSEA-1 by immunofluorescence. Passage 35. This line is a
                     subclone of the parental line; the parental line was
                     subcloned to remove aneuploid cells). cDNA was primed
                     using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
                     kb resulted in an average insert size of 1.9 kb. This
                     primary library is non-normalized (normalized primary
                     library is NIH_MGC_279) and was constructed by Express
                     Genomics (Frederick, MD). Note: this is a Mammalian Gene
                     Collection library."
ORIGIN
```

Query Match 54.9%; Score 656.2; DB 8; Length 742;
Best Local Similarity 97.4%; Pred. No. 2.2e-141;
Matches 667; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              | |||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||
Db         58 CTGAGACTCACGGTCAAGCTACGGCGAGGAGTGGGTGGCTGAAGCCATACTATTTTATAG 117

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              |||||||||||||||||||| |||||||||||||||| |||||||||||||||||||||
Db        118 AATTAATGGAAAGCAGAAAAGACGTCACAAACCAAGAAGAAATTTGGAAAATGAAGCCTA 177

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||  |||||||||||||||||||||||||||||||||||||||||||
Db        178 GGAGAAATTTAGAAGACAACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 237

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        238 AAAGACCTGTGCTTTTGCATTTGCAGCGAACAGCCCATGCTGATGAATTTGACTGCCCTT 297

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 357

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              || |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 CTGTTATGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 417

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 CAACTTCCCGTCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 477

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              || |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        478 CAGTGGTTTCCATCACTCTCTTGGCATTGGTTTACCTACCAGGTGTGATAGCAGCAATTG 537

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 597

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 657

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              |||||||||| |||||| ||||||||||||||||||||||||||||||||||||||||||
Db        658 CTCTGTCTTACGCAATGATGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 717

Qy        661 AGGTCCAACAAAATAAAGAAGATGC 685
              ||||||||||||| ||||||||||
Db        718 AGGTCCAACAAAATGAAGAAGATGC 742
```

```
RESULT 14
BI552907
LOCUS       BI552907                783 bp    mRNA    linear   EST 05-SEP-2001
DEFINITION  603197827F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277295 5',
            mRNA sequence.
ACCESSION   BI552907
VERSION     BI552907.1  GI:15440219
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 783)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11700  row: e  column: 08
            High quality sequence stop: 769.
FEATURES             Location/Qualifiers
     source          1. .783
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5277295"
                     /tissue_type="hippocampus"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_95"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI
```

(gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3', size-selected for average insert size 2.5 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

ORIGIN

```
  Query Match             54.8%;  Score 655;  DB 3;  Length 783;
  Best Local Similarity   99.0%;  Pred. No. 4.2e-141;
  Matches  680;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         97 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 156

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        157 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 216

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        217 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 276

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        277 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 336

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        337 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 396

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 456

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 516

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        517 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 576

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 636

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCA-TGCAATTTAT 599
              |||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        637 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTCTGCTGTACTGCATTGCAATTTAT 696

Qy        600 AGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACT-GGGCATATCA 658
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        697 AGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGGCATATCA 756

Qy        659 ACAGGTCCAACAAAATAAAGAAGATGC 685
              |||||||||||||  ||  ||||||||
Db        757 CCAGGTCCAACAAACTACCGAAGATGC 783
```

RESULT 15
CX753134
LOCUS CX753134 825 bp mRNA linear EST 24-JAN-2005
DEFINITION AGENCOURT_40991781 NIH_MGC_281 Homo sapiens cDNA clone IMAGE:7780881 3', mRNA sequence.
ACCESSION CX753134
VERSION CX753134.1 GI:58049789
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 825)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Meri Firpo
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15937 row: a column: 07
High quality sequence stop: 538.

FEATURES Location/Qualifiers
source 1. .825
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:7780881"
/tissue_type="pluripotent cell line derived from blastocyst inner cell mass"
/lab_host="DH10B TonA"
/clone_lib="NIH_MGC_281"
/note="Organ: Blastocyst; Vector: pExpress-1; Site_1: EcoRV; Site_2: NotI; RNA obtained from pluripotent cell line derived from blastocyst inner cell mass (cell line HSF-6, NIH Registry designation UC06. Positive for OCT4 expression by rtPCR, positive for SSEA-3, SSEA-4, Tra-1-81, Tra-1-60 by immunofluorescence. Negative for SSEA-1 by immunofluorescence Passage 62. cDNA was primed using oligo-dT primer: 5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25 kb resulted in an average insert size of 2.0 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_280) and was constructed by Express Genomics (Frederick, MD). Note: this is a Mammalian Gene Collection library."

ORIGIN

```
  Query Match             54.8%;  Score 654.6;  DB 8;  Length 825;
  Best Local Similarity   98.5%;  Pred. No. 5.2e-141;
  Matches  671;  Conservative    0;  Mismatches    9;  Indels    1;  Gaps    1;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 124

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 184

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 244

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 304

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 364

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
```

```
Db        365 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 424

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 484

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        485 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 544

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 604

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 664

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||| |||||||||| ||||||||||||| || ||||||||||||||||||||||||
Db        665 GTCTGTCCTACCCAATGAAGCGATCCTACAGA-ACCAGTTGCTAAACTGGGCATATCAAC 723

Qy        661 AGGTCCAACAAAATAAAGAAG 681
              ||||| |  || | ||||| |
Db        724 AGGTCAACAAATAAAAAGATG 744
```

Search completed: December 5, 2005, 03:12:12
Job time : 5464.54 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:13:31 ; Search time 802.249 Seconds
(without alignments)
9927.475 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactcacggtcaagct.....ggaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1195	100.0	1195	4	AAH93924	Aah93924 P789P ful
2	1195	100.0	1195	4	AAS64160	Aas64160 Human pro
3	1195	100.0	1195	5	ACA59968	Aca59968 Prostate
4	1195	100.0	1195	6	ABL95531	Abl95531 Human P78
5	1195	100.0	1195	6	ABK92128	Abk92128 Prostate
6	1195	100.0	1195	8	ACC95695	Acc95695 Prostate
7	1195	100.0	1195	10	ADB75572	Adb75572 Prostate
8	1195	100.0	1195	10	ADB14328	Adb14328 Human pro
9	1195	100.0	1195	10	AAD63162	Aad63162 Human STE
10	1195	100.0	1195	10	AAD62763	Aad62763 Human STE
11	1195	100.0	1195	10	ADG26744	Adg26744 Human pro
12	1195	100.0	1195	11	ADN39812	Adn39812 Cancer/an
13	1195	100.0	1195	11	ADN39395	Adn39395 Cancer/an
14	1195	100.0	1195	11	ADP88258	Adp88258 Prostate
15	1195	100.0	1195	12	ADL06462	Adl06462 Human tum
16	1195	100.0	1195	12	ADL06436	Adl06436 Human tum
17	1195	100.0	1195	12	ADJ75176	Adj75176 Marker ge
18	1195	100.0	1330	13	ADR14190	Adr14190 Human NF-
19	1195	100.0	1330	13	ADU06030	Adu06030 Novel bro
20	1195	100.0	1330	14	ADY15575	Ady15575 DNA encod
21	1195	100.0	1330	14	ADY19959	Ady19959 DNA encod
22	1193	99.8	1193	3	AAZ49395	Aaz49395 Human STR
23	1193	99.8	1193	5	AAD07067	Aad07067 Human six
24	1193	99.8	1193	14	ADY92698	Ady92698 Human STE
25	1190	99.6	1294	4	AAK51978	Aak51978 Human pol
26	1182	98.9	1198	8	ACD02628	Acd02628 STEAP-1 v
27	1181.8	98.9	1193	8	ACD02597	Acd02597 cDNA enco
28	1180.4	98.8	1198	8	ACD02629	Acd02629 STEAP-1 v
29	1178	98.6	1277	5	ADL46020	Adl46020 Human ova
30	1177	98.5	1177	14	ADV73174	Adv73174 Human col
31	1177	98.5	1201	13	ADX33625	Adx33625 Plant ful
32	1174.4	98.3	1229	4	AAK52962	Aak52962 Human pol
33	1166	97.6	1354	12	ADQ22300	Adq22300 Human sof
34	1048	87.7	1365	8	ACD02599	Acd02599 cDNA enco
35	1048	87.7	1365	8	ACD02630	Acd02630 STEAP-1 v
36	1044	87.4	1369	8	ACD02632	Acd02632 STEAP-1 v
37	1042.4	87.2	1369	8	ACD02631	Acd02631 STEAP-1 v
38	827.2	69.2	3627	8	ACD02601	Acd02601 cDNA enco
39	825.6	69.1	3627	3	AAZ49396	Aaz49396 Human STR
40	825.6	69.1	3627	5	AAD07071	Aad07071 Human six
41	825.6	69.1	3627	8	ACD02613	Acd02613 cDNA enco
42	825.6	69.1	3627	8	ACD02605	Acd02605 cDNA enco
43	825.6	69.1	3627	8	ACD02606	Acd02606 cDNA enco
44	825.6	69.1	3627	8	ACD02598	Acd02598 cDNA enco
45	825.6	69.1	3627	8	ACD02612	Acd02612 cDNA enco

ALIGNMENTS

RESULT 1
AAH93924
ID AAH93924 standard; cDNA; 1195 BP.
XX
AC AAH93924;
XX
DT 04-OCT-2001 (first entry)
XX
DE P789P full length cDNA sequence.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
PS Claim 1; Page 510; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used treat cancer in a patient. (I) and

```
CC   the antibodies are also used in the detection of cancer in a patient. The
CC   cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC   and (II) can be used in vaccines. The antibodies or (I) can be used for
CC   monitoring the progression of cancer in a patient. (I) and (II) can also
CC   be used to improve diagnostic and therapeutic methods for prostate
CC   cancer. They can indicate the level of metastasis as well as the prostate
CC   volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC   polynucleotide and amino acid sequences used in the exemplification of
CC   the present invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1195;  DB 4;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 2
AAS64160
ID   AAS64160 standard; cDNA; 1195 BP.
XX
AC   AAS64160;
XX
DT   29-JAN-2002  (first entry)
XX
DE   Human prostate cDNA sequence #590.
XX
KW   Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200173032-A2.
XX
PD   04-OCT-2001.
XX
PF   27-MAR-2001; 2001WO-US009919.
XX
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-00709729.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Kalos MD;
PI   Fanger GR,  Retter MW,  Stolk JA,  Day CH,  Vedvick TS,  Carter D;
PI   Li SX,  Wang A,  Skeiky YAW,  Hepler WT,  Henderson RA;
XX
DR   WPI; 2001-639232/73.
DR   P-PSDB; AAU69927.
XX
PT   New human prostate-specific polypeptides and polynucleotides useful for
PT   the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS   Claim 1; Page 548; 579pp; English.
XX
CC   The invention relates to isolated prostate-specific polynucleotides,
CC   polypeptides, fusion proteins of the polypeptides, antibodies raised
CC   against the polypeptides (or antigenic epitopes derived from them) and
```

```
CC   antigen-presenting cells expressing the polypeptides. The antibodies are
CC   useful for detecting the presence of cancer, especially prostate cancer.
CC   The polypeptides, polynucleotides and the antigen-presenting cells are
CC   useful for stimulating and/or expanding T cells specific for a tumour
CC   protein, and for inhibiting the development of cancer especially prostate
CC   cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC   useful for stimulating an immune response, and for treating cancer. The
CC   oligonucleotide is useful for detecting cancer. The present sequence is a
CC   prostate specific polynucleotide of the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1195;  DB 4;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 3
ACA59968
ID   ACA59968 standard; cDNA; 1195 BP.
XX
AC   ACA59968;
XX
DT   10-JUN-2003  (first entry)
XX
DE   Prostate cancer therapy associated cDNA #655.
XX
KW   Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW   immunogen; cancer; prostate specific antigen; PSA;
KW   prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW   PSMA; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002192763-A1.
XX
PD   19-DEC-2002.
XX
PF   29-JUN-2001; 2001US-00895793.
XX
PR   04-OCT-1999;   99US-0157455P.
PR   04-OCT-2000; 2000US-00679272.
PR   28-MAR-2001; 2001US-00822827.
XX
PA   (XUJJ/) XU J.
PA   (DILL/) DILLON D C.
PA   (MITC/) MITCHAM J L.
PA   (HARL/) HARLOCKER S L.
PA   (JIAN/) JIANG Y.
PA   (KALO/) KALOS M D.
PA   (FANG/) FANGER G R.
PA   (RETT/) RETTER M W.
PA   (STOL/) STOLK J A.
PA   (DAYC/) DAY C H.
PA   (VEDV/) VEDVICK T S.
PA   (CART/) CARTER D.
PA   (LISX/) LI S X.
PA   (WANG/) WANG A.
PA   (SKEI/) SKEIKY Y A W.
PA   (HEPL/) HEPLER W T.
PA   (HEND/) HENDERSON R A.
PA   (HURA/) HURAL J.
PA   (MCNE/) MCNEILL P D.
PA   (HOUG/) HOUGHTON R L.
PA   (DBAS/) Y DE BASSOLS C V.
PA   (FOYT/) FOY T M.
```

```
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Kalos MD;
PI   Fanger GR,  Retter MW,  Stolk JA,  Day CH,  Vedvick TS,  Carter D;
PI   Li SX,  Wang A,  Skeiky YAW,  Hepler WT,  Henderson RA,  Hural J;
PI   Mcneill PD,  Houghton RL,  Y De BassolsCV,  Foy TM;
XX
DR   WPI; 2001-245062/25.
DR   P-PSDB; ABU71821.
XX
PT   Prostate specific protein and its encoding polynucleotide, useful for the
PT   treatment and diagnosis of prostate cancer.
XX
PS   Example 5; SEQ ID NO 878; 85pp; English.
XX
CC   The invention describes a fusion protein comprising at least one amino
CC   acid sequence of immunogenic portions of any of the 3 sequences not
CC   defined in the specification, or sequences having at least 70 or 90 %
CC   sequence identity to any one of the 35 sequences defined in the USPTO web
CC   site, which is encoded by any of the 4 nucleotide sequences not defined
CC   in the specification. The fusion protein, composition and methods are
CC   useful for diagnosing, preventing and/or treating cancer, particularly
CC   prostate cancer. The proteins are useful as markers to indicate the
CC   presence or absence of cancer. This sequence represents a prostate cancer
CC   therapy associated cDNA. Note: The sequence data for this patent did not
CC   form part of the printed specification, but was obtained in electronic
CC   format directly from the US patent office at
CC   seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1195;  DB 5;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 4
ABL95531
ID   ABL95531 standard; cDNA; 1195 BP.
XX
AC   ABL95531;
XX
DT   19-JUL-2002  (first entry)
XX
DE   Human P789P cDNA sequence SEQ ID NO 878.
XX
KW   Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW   gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2002022248-A1.
XX
PD   21-FEB-2002.
XX
PF   12-JAN-2001; 2001US-00759143.
XX
PR   25-FEB-1997;   97US-00806099.
PR   01-AUG-1997;   97US-00904804.
PR   10-FEB-1998;   98US-00020956.
PR   25-FEB-1998;   98US-00030607.
PR   14-JUL-1998;   98US-00115453.
PR   23-SEP-1998;   98US-00159812.
PR   15-JAN-1999;   99US-00232149.
PR   09-APR-1999;   99US-00288946.
PR   13-JUL-1999;   99US-00352616.
PR   12-NOV-1999;   99US-00439313.
```

```
PR   18-NOV-1999;   99US-00443686.
PR   14-JAN-2000; 2000US-00483672.
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   10-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
XX
PA   (XUJJ/) XU J.
PA   (DILL/) DILLON D C.
PA   (MITC/) MITCHAM J L.
PA   (HARL/) HARLOCKER S L.
PA   (JIAN/) JIANG Y.
PA   (KALO/) KALOS M D.
PA   (FANG/) FANGER G R.
PA   (RETT/) RETTER M W.
PA   (STOL/) STOLK J A.
PA   (DAYC/) DAY C H.
PA   (VEDV/) VEDVICK T S.
PA   (CART/) CARTER D.
PA   (LISX/) LI S X.
PA   (WANG/) WANG A.
PA   (SKEI/) SKEIKY Y A W.
PA   (HEPL/) HEPLER W T.
PA   (HEND/) HENDERSON R A.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Kalos MD;
PI   Fanger GR,  Retter MW,  Stolk JA,  Day CH,  Vedvick TS,  Carter D;
PI   Li SX,  Wang A,  Skeiky YAW,  Hepler WT,  Henderson RA;
XX
DR   WPI; 2002-255649/30.
XX
PT   New prostate-specific polynucleotides for diagnosing and treating
PT   diseases, in particular prostate cancer, and as markers for the
PT   progression of cancer.
XX
PS   Claim 1; SEQ ID NO 878; 87pp; English.
XX
CC   The present invention provides prostate-specific coding sequences and
CC   their encoded proteins. These can be used in the diagnosis and treatment
CC   of cancers, particularly prostate cancer. The present sequence is a cDNA
CC   described in the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 5
ABK92128
ID   ABK92128 standard; DNA; 1195 BP.
XX
AC   ABK92128;
XX
DT   15-AUG-2002  (first entry)
XX
DE   Prostate cancer-associated DNA sequence #14.
XX
KW   Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
```

KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61813.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 311-312; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

RESULT 6
ACC95695
ID ACC95695 standard; cDNA; 1195 BP.
XX
AC ACC95695;
XX
DT 28-AUG-2003 (first entry)

```
XX
DE   Prostate tumour specific cDNA sequence SEQ ID 878.
XX
KW   Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW   immune response; prostate cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200289747-A2.
XX
PD   14-NOV-2002.
XX
PF   09-MAY-2002; 2002WO-US014753.
XX
PR   09-MAY-2001; 2001US-00852911.
PR   29-JUN-2001; 2001US-00895814.
PR   10-DEC-2001; 2001US-00012896.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Dillon DC,  Mitcham JL,  Harlocker SL,  Jiang Y,  Henderson RA;
PI   Kalos MD,  Fanger GR,  Retter MW,  Stolk JA,  Day CH,  Vedvick TS;
PI   Carter D,  Li SX,  Wang A,  Skeiky YAW,  Hepler WT,  Hural J;
PI   Mcneill PD,  Houghton RL,  Vinals Y De BassolsC,  Foy TM,  Watanabe Y;
PI   Deng T;
XX
DR   WPI; 2003-167130/16.
XX
PT   New prostate-specific proteins and genes, useful in gene therapy,
PT   particularly for stimulating an immune response in a patient, or treating
PT   prostate cancer in a patient, as well as for diagnosing prostate cancer
PT   in a patient.
XX
PS   Example 5; Page 617-618; 691pp; English.
XX
CC   The present invention relates to novel prostate-specific proteins (PSP)
CC   and their coding sequences. The PSPs and their coding sequences are
CC   useful for stimulating an immune response in a patient, or for treating
CC   prostate cancer in a patient and for determining, detecting or diagnosing
CC   the presence of a cancer in a patient. The present sequence was used to
CC   illustrate the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1195;  DB 8;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 7
ADB75572
ID   ADB75572 standard; cDNA; 1195 BP.
XX
AC   ADB75572;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Prostate cancer marker cDNA.
XX
KW   Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003009814-A2.
XX
PD   06-FEB-2003.
```

XX
PF 25-JUL-2002; 2002WO-US023913.
XX
PR 25-JUL-2001; 2001US-0307982P.
PR 22-AUG-2001; 2001US-0314356P.
PR 25-SEP-2001; 2001US-0325020P.
PR 12-DEC-2001; 2001US-0341746P.
PR 05-MAR-2002; 2002US-0362158P.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbatcheva B;
PI Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
DR WPI; 2003-248033/24.
XX
PT New nucleic acid molecule, useful for diagnosing or treating prostate
PT cancer.
XX
PS Disclosure; SEQ ID NO 396; 99pp; English.
XX
CC The invention relates to newly discovered cancer markers associated with
CC the cancerous state of prostate cells. Also disclosed is a method of
CC assessing whether a patient is afflicted with prostate cancer. The method
CC of the invention involves assessing whether a patient is afflicted with
CC prostate cancer by comparing the level of expression of a marker in a
CC patient sample and the normal level of expression of the marker in a
CC control non-prostate cancer sample, where a significant increase in the
CC level of expression of the marker in the patient sample and the normal
CC level indicates that the patient is afflicted with prostate cancer.
CC Nucleic acids of the invention are useful for diagnosing or treating
CC prostate cancer, and may be useful in gene therapy. Sequences given in
CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
```

RESULT 8
ADB14328
ID ADB14328 standard; cDNA; 1195 BP.
XX
AC ADB14328;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific full length cDNA P789P.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.

```
XX
PR   25-FEB-1997;   97US-00806099.
PR   01-AUG-1997;   97US-00904804.
PR   09-FEB-1998;   98US-00020956.
PR   25-FEB-1998;   98US-00030607.
PR   14-JUL-1998;   98US-00115453.
PR   23-SEP-1998;   98US-00159812.
PR   15-JAN-1999;   99US-00232149.
PR   09-APR-1999;   99US-00288946.
PR   13-JUL-1999;   99US-00352616.
PR   12-NOV-1999;   99US-00439313.
PR   18-NOV-1999;   99US-00443686.
PR   14-JAN-2000; 2000US-00483672.
PR   27-MAR-2000; 2000US-00536857.
PR   09-MAY-2000; 2000US-00568100.
PR   12-MAY-2000; 2000US-00570737.
PR   13-JUN-2000; 2000US-00593793.
PR   27-JUN-2000; 2000US-00605783.
PR   09-AUG-2000; 2000US-00636215.
PR   29-AUG-2000; 2000US-00651236.
PR   06-SEP-2000; 2000US-00657279.
PR   02-OCT-2000; 2000US-00679426.
PR   10-OCT-2000; 2000US-00685166.
PR   09-NOV-2000; 2000US-00709729.
PR   12-JAN-2001; 2001US-00759143.
PR   09-FEB-2001; 2001US-00780669.
PR   09-MAY-2001; 2001US-00852911.
PR   29-JUN-2001; 2001US-00895814.
PR   10-DEC-2001; 2001US-00012896.
PR   09-MAY-2002; 2002US-00144678.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Xu J,  Stolk JA,  Kalos MD;
XX
DR   WPI; 2003-756193/71.
DR   P-PSDB; ADB14329.
XX
PT   New isolated polypeptide for use in a vaccine for stimulating an immune
PT   response, or for treating or diagnosis cancer, preferably prostate
PT   cancer.
XX
PS   Example 5; Page; 101pp; English.
XX
CC   The invention relates to an isolated polypeptide comprising no more than
CC   11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC   peptides comprise a fragment ADB13563 of that contain naturally processed
CC   T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC   alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC   cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC   encoding the proteins and peptides, expression vectors, a host cell
CC   transformed with the vector, an isolated antibody (or antigen binding
CC   fragment) that specifically binds to the protein or peptide, detecting
CC   the presence of a cancer in a patient (comprising contacting a patient
CC   sample with a binding agent that binds to the peptides or a polypeptide
CC   appearing as ADB13558, detecting the amount of polypeptide that binds to
CC   the agent and comparing the amount of polypeptide to a predetermined cut-
CC   off value to determine the presence of cancer), a fusion protein
CC   comprising the peptides or proteins, stimulating or expanding T cells
CC   specific for a tumour protein comprising contacting T cells with the
CC   peptides or the isolated T cell population, treating prostate cancer in a
CC   patient comprising administering a composition comprising the peptides,
CC   nucleic acids, antibodies or compounds, determining the presence of a
CC   cancer in a patient and treating prostate cancer in a patient comprising
CC   incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC   from a patient with the peptides or antigen presenting cells that express
CC   (the peptides so that the T cells proliferate, and administering the
CC   proliferated T cells to the patient. The peptides (or an oligonucleotide
CC   that hybridises to nucleic acid encoding them), is used to detect the
CC   presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC   antigen-presenting cells expressing the nucleic acid, are used to
CC   stimulate or expand T cells specific for a tumour protein. The peptides,
CC   nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC   presenting cells are used to stimulate an immune response or treat
CC   prostate cancer in a patient. The present sequence is a known cDNA
CC   showing sequence similarity to one of the disclosed human prostate
CC   specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1195;  DB 10;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
```

```
Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

RESULT 9
AAD63162
ID AAD63162 standard; DNA; 1195 BP.
XX
AC AAD63162;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
KW Human; breast cancer; metastasis; differential modulation; therapy;
KW STEAP; six transmembrane epithelial antigen of the prostate; ds.
XX
OS Homo sapiens.
XX
PN US2003190656-A1.
XX
PD 09-OCT-2003.
XX
PF 21-MAR-2003; 2003US-00393590.
XX
PR 29-MAR-2002; 2002US-0368789P.
XX
PA (WANG/) WANG Y.
XX
PI Wang Y;
XX
DR WPI; 2003-831621/77.
XX
PT Prognosticating metastasis in a breast cancer patient comprises
PT identifying differential modulation of each gene relative to the
PT expression of the same genes in a normal population in combination of
PT genes.
XX
PS Example 2; Page 54-55; 0pp; English.
XX
CC The present invention relates to a method of prognosticating metastasis
CC in a breast cancer patient involves identifying differential modulation
CC of each gene relative to the expression of the same genes in a normal
CC population in combination of genes. The invention is useful for
CC prognosticating breast cancer in a patient. The present sequence is human
CC STEAP (six transmembrane epithelial antigen of the prostate) DNA used to
CC illustrate the method of the invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 10
AAD62763
ID   AAD62763 standard; DNA; 1195 BP.
XX
AC   AAD62763;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
KW   Human; cancer; differential modulation; gene expression profile; STEAP;
KW   six transmembrane epithelial antigen of the prostate; ds.
XX
OS   Homo sapiens.
XX
PN   US2003194733-A1.
XX
PD   16-OCT-2003.
XX
PF   21-MAR-2003; 2003US-00393567.
XX
PR   29-MAR-2002; 2002US-0368667P.
XX
PA   (WANG/) WANG Y.
XX
PI   Wang Y;
XX
DR   WPI; 2003-844450/78.
XX
PT   Diagnosing cancer comprises identifying differential modulation of each
PT   gene (relative to the expression of the same genes in a normal
PT   population) in a combination of genes.
XX
PS   Claim 4; Page 54-55; 0pp; English.
XX
CC   The invention relates to a method for diagnosing cancer. The method
CC   comprising identifying differential modulation of each gene (relative to
CC   the expression of the same genes in a normal population) in a combination
CC   of genes. The method, diagnostic portfolio and the kit are useful in
CC   diagnosing cancer. The method may also be used for determining gene
CC   expression profiles. The present sequence is human STEAP (six
CC   transmembrane epithelial antigen of the prostate) DNA used to illustrate
CC   the method of the invention
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1195;  DB 10;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 11
ADG26744
ID   ADG26744 standard; cDNA; 1195 BP.
XX
AC   ADG26744;
XX
DT   26-FEB-2004  (first entry)
XX
```

DE Human prostate-specific cDNA #678.
XX
KW Human; prostate-specific polypeptide; gene; ss; prostate cancer;
KW cytostatic.
XX
OS Homo sapiens.
XX
PN US2003157089-A1.
XX
PD 21-AUG-2003.
XX
PF 09-MAY-2002; 2002US-00144678.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Meagher MJ, Deng T;
XX
DR WPI; 2003-777973/73.
DR P-PSDB; ADG26745.
XX
PT New polynucleotides encoding prostate specific polypeptides isolated from
PT a human prostate tumor cDNA library are useful to diagnose and treat
PT cancer particularly prostate cancer.
XX
PS Example 5; SEQ ID NO 878; 99pp; English.
XX
CC The invention relates to human prostate-specific polypeptides and the
CC polynucleotides encoding them. The invention also relates to an isolated
CC antibody or its antigen-binding fragment that specifically binds a
CC polypeptide of the invention, a method of detecting cancer in a patient
CC comprising contacting a biological sample of the patient with an agent
CC that binds a prostate-specific polypeptide and comparing the amount of
CC bound polypeptide compared to a predetermined cut-off value and a fusion
CC protein comprising a prostate-specific polypeptide. The sequences of the
CC invention are used to diagnose and treat cancer, particularly prostate
CC cancer. This sequence represents cDNA encoding a human prostate-specific
CC polypeptide of the invention. Note: The sequence data for this patent did
CC not form part of the printed specification but was obtained in electronic
CC format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 10; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
```

```
Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

RESULT 12
ADN39812
ID ADN39812 standard; cDNA; 1195 BP.
XX
AC ADN39812;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:C184.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnerary; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR P-PSDB; ADN40029.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 8; SEQ ID NO C184; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 11; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

RESULT 13
ADN39395
ID ADN39395 standard; cDNA; 1195 BP.
XX
AC ADN39395;
XX
DT 17-JUN-2004 (first entry)
XX
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:B79.
XX
KW Human; differential expression; cancer; angiogenic disorder;
KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
KW inflammatory disease; autoimmune disease;
KW retinal neovascularistaion syndrome; scarring; uterine fibroid;
KW detection; diagnosis; prognosis; drug screening; drug targeting;
KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;
KW vulnerary; gene therapy; vaccine; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2003042661-A2.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2002; 2002WO-US036810.
XX
PR 13-NOV-2001; 2001US-0350666P.
PR 21-NOV-2001; 2001US-0332464P.
PR 29-NOV-2001; 2001US-0334393P.
PR 03-DEC-2001; 2001US-0335394P.
PR 14-DEC-2001; 2001US-0340376P.
PR 08-JAN-2002; 2002US-0347211P.
PR 10-JAN-2002; 2002US-0347349P.
PR 08-FEB-2002; 2002US-0355250P.
PR 13-FEB-2002; 2002US-0356714P.
PR 20-FEB-2002; 2002US-0359077P.
PR 29-MAR-2002; 2002US-0368809P.
PR 04-APR-2002; 2002US-0370110P.
PR 12-APR-2002; 2002US-0372246P.
PR 05-JUN-2002; 2002US-0386614P.
PR 16-JUL-2002; 2002US-0396839P.
PR 22-JUL-2002; 2002US-0397775P.
PR 22-JUL-2002; 2002US-0397845P.
PR 09-SEP-2002; 2002US-0409450P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynne R, Hevezi PA;
PI Mack DH, Murray R, Watson SR, Wilson KE, Zlotnik A;
XX
DR WPI; 2003-468649/44.
DR P-PSDB; ADN39396.
XX
PT Determining the presence or absence of a pathological cell in a patient,
PT useful for diagnosing, prognosing or treating cancer, comprises detecting
PT a nucleic acid in a biological sample.
XX
PS Claim 8; SEQ ID NO B79; 1385pp; English.
XX
CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064)
CC whose expression is upregulated or downregulated in specific cancers or
CC other diseases such as angiogenic or fibrotic disorders, and to methods
CC of determining the presence or absence of a pathological cell in a
CC patient by detecting a nucleic acid at least 80% identical to those of
CC the invention or by detecting a polypeptide of the invention. The
CC invention also relates to expression vectors and host cells comprising a
CC nucleic acid of the invention; antibodies which specifically bind a
CC polypeptide of the invention; use of such antibodies for drug targeting;
CC and methods of screening for modulators of activity or expression of the
CC polypeptides and nucleic acids. The nucleic acids, polypeptides,
CC antibodies and methods are useful for diagnosing, prognosing and treating
CC cancer and other conditions such as psoriasis, ischaemia, heart disease,
CC atherosclerosis, inflammatory diseases, autoimmune diseases, retinal
CC neovascularistaion syndromes, scarring and uterine fibroids. They may
CC also be useful in wound healing and in contraception. The present
CC sequence represents a nucleic acid sequence of the invention.
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 11; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
```

```
Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 14
ADP88258
ID   ADP88258 standard; cDNA; 1195 BP.
XX
AC   ADP88258;
XX
DT   12-AUG-2004  (first entry)
XX
DE   Prostate cancer marker gene STEAP, SEQ ID NO:35.
XX
KW   Diagnostic marker; portfolio; diagnostic parameter; gene expression;
KW   relative expression; heuristic rule; molecular diagnostic; diagnosis;
KW   prognosis; cancer; breast; prostate; ovarian; colorectal; lung;
KW   screening portfolio; human; STEAP; gene; ss.
XX
OS   Homo sapiens.
XX
PN   EP1349104-A2.
XX
PD   01-OCT-2003.
XX
PF   31-MAR-2003; 2003EP-00252027.
XX
PR   29-MAR-2002; 2002US-0368790P.
XX
PA   (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
XX
PI   Jatkoe T;
XX
DR   WPI; 2003-815043/77.
XX
PT   Selecting a portfolio of markers useful in diagnostic applications
PT   comprises defining diagnostic parameters and establishing a relationship
PT   among the diagnostic parameters that identifies an optimized portfolio of
PT   markers.
XX
PS   Example 2; SEQ ID NO 35; 154pp; English.
XX
CC   The invention relates to a method of selecting a portfolio of markers
CC   (e.g., genes) for use in a diagnostic application. The method involves:
CC   (a) defining diagnostic parameters; (b) establishing a relationship among
CC   the diagnostic parameters so that they are optimised; and (c) selecting
CC   the optimal group of markers (the portfolio) for the diagnostic
CC   application. The diagnostic parameters can include a measure of the
CC   relative degree of expression of a gene, a measure of the variation in
CC   the measurement of the degree of gene expression, and the relationship
CC   between the diagnostic and discriminating parameters can be a mean
CC   variance relationship. The method further comprises the application of a
CC   heuristic rule. The invention also relates to a general-purpose computer
CC   programmed to identify a portfolio of markers, instructions for
CC   performing the method of the invention, and a diagnostic portfolio
CC   comprising genes selected according to the method. The method of the
CC   invention can be used in conjunction with any method for determining the
CC   gene expression of relevant cells as well as protein-based methods of
CC   determining gene expression. The method of the invention can be used in
CC   screening, diagnosing and prognosing diseases associated with changes in
CC   the expression of multiple genes (e.g., breast, prostate, ovarian,
CC   colorectal or lung cancer). By grouping these markers into portfolios,
CC   the most reliable results can be obtained with the smallest number of
CC   markers necessary to obtain such a result, which is particularly
CC   important in multiple-step assays such as nucleic amplification methods.
CC   The present sequence represents a human diagnostic marker gene that is a
CC   member of an optimised portfolio of 31 genes for screening for prostate,
CC   breast, colon, ovarian and lung cancer.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1195;  DB 11;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-276;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
```

```
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

RESULT 15
ADL06462
ID ADL06462 standard; cDNA; 1195 BP.
XX
AC ADL06462;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human tumour-associated antigenic target (TAT) cDNA sequence #42.
XX
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;
KW cancer; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
PN WO2004016225-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025892.
XX
PR 19-AUG-2002; 2002US-0404809P.
PR 21-AUG-2002; 2002US-0405645P.
PR 23-SEP-2002; 2002US-0413192P.
PR 15-OCT-2002; 2002US-0419008P.
PR 15-NOV-2002; 2002US-0426847P.
PR 02-JUL-2003; 2003US-0484959P.
XX
PA (GETH) GENENTECH INC.
XX
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;
PI Spencer SD, Wu TD, Zhang Z;
XX
DR WPI; 2004-257144/24.
DR P-PSDB; ADL06542.
XX
PT New antibody that binds to a tumor-associated antigenic target (TAT)
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating cancer.
XX
PS Claim 1; SEQ ID NO 42; 319pp; English.
XX
CC The present invention relates to the isolation of human tumour-associated
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is
CC produced in bacteria or in CHO cells and induces death of a cell to which
CC it binds. The antibody is useful for preparing a composition for
CC diagnosing or treating tumours and cancer. The present sequence
CC represents a human TAT cDNA sequence of the invention.
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1195; DB 12; Length 1195;
Best Local Similarity 100.0%; Pred. No. 4.4e-276;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
```

```
Qy       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy       541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy       661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy       721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy       781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy       841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy       901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy       961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy      1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy      1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

Search completed: December 4, 2005, 21:08:41
Job time : 807.249 secs

This Page Intentionally Left Blank

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:37:01 ; Search time 6316.97 Seconds
(without alignments)
10753.247 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactcacggtcaagct.....ggaaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1195	100.0	1195	6	CQ776742	CQ776742 Sequence
2	1195	100.0	1195	6	AR366780	AR366780 Sequence
3	1195	100.0	1195	6	AR405830	AR405830 Sequence
4	1195	100.0	1195	6	AR564210	AR564210 Sequence
5	1195	100.0	1195	6	AR589196	AR589196 Sequence
6	1195	100.0	1195	6	AR654075	AR654075 Sequence
7	1195	100.0	1195	6	AX201105	AX201105 Sequence
8	1195	100.0	1195	6	AX267904	AX267904 Sequence
9	1195	100.0	1195	6	AX926483	AX926483 Sequence
10	1195	100.0	1195	6	AX951736	AX951736 Sequence
11	1195	100.0	1195	6	AX960014	AX960014 Sequence
12	1195	100.0	1195	8	AF186249	AF186249 Homo sapi
13	1195	100.0	1330	6	CQ981397	CQ981397 Sequence
14	1195	100.0	1330	6	CS031875	CS031875 Sequence
15	1195	100.0	1330	6	CS036259	CS036259 Sequence
16	1195	100.0	1330	6	CS040827	CS040827 Sequence
17	1195	100.0	1330	6	CS045211	CS045211 Sequence
18	1193	99.8	1193	6	BD232184	BD232184 Novel ser
19	1193	99.8	1193	6	AR617054	AR617054 Sequence
20	1193	99.8	1193	6	AX155243	AX155243 Sequence
21	1191.8	99.7	1240	8	BC011802	BC011802 Homo sapi
22	1178	98.6	1277	6	CQ412839	CQ412839 Sequence
23	946.6	79.2	1754	4	AF319659	AF319659 Sus scrof
24	825.6	69.1	3627	6	BD232188	BD232188 Novel ser
25	825.6	69.1	3627	6	AR366784	AR366784 Sequence
26	825.6	69.1	3627	6	AR617056	AR617056 Sequence
27	825.6	69.1	3627	6	AR654079	AR654079 Sequence
28	825.6	69.1	3627	6	AX155248	AX155248 Sequence
29	810.2	67.8	1234	9	BC061023	BC061023 Mus muscu
30	809.6	67.7	1175	9	AF297098	AF297098 Mus muscu
31	806	67.4	1211	6	CQ777614	CQ777614 Sequence
32	759.6	63.6	1198	6	BD192004	BD192004 Modulator
33	712	59.6	1191	9	AY029584	AY029584 Mus muscu
34	675.8	56.6	1209	8	BC066301	BC066301 Homo sapi
c 35	581	48.6	592	6	BD242240	BD242240 Compounds
c 36	581	48.6	592	6	AR278447	AR278447 Sequence
c 37	581	48.6	592	6	AR367143	AR367143 Sequence
c 38	581	48.6	592	6	AR371039	AR371039 Sequence
c 39	581	48.6	592	6	AR400179	AR400179 Sequence
c 40	581	48.6	592	6	AR405446	AR405446 Sequence
c 41	581	48.6	592	6	AR563826	AR563826 Sequence
c 42	581	48.6	592	6	AR588812	AR588812 Sequence
c 43	581	48.6	592	6	AR605632	AR605632 Sequence
c 44	581	48.6	592	6	AR656971	AR656971 Sequence
c 45	581	48.6	592	6	AX106561	AX106561 Sequence

ALIGNMENTS

RESULT 1
CQ776742
LOCUS CQ776742 1195 bp DNA linear PAT 11-MAR-2004
DEFINITION Sequence 428 from Patent EP1394274.
ACCESSION CQ776742
VERSION CQ776742.1 GI:45380132
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
TITLE Methods of testing for bronchial asthma or chronic obstructive pulmonary disease
JOURNAL Patent: EP 1394274-A 428 03-MAR-2004;
Genox Research, Inc. (JP)
FEATURES Location/Qualifiers
source 1. .1195
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 1195; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 5.5e-238;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
```

```
Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 2
AR366780
LOCUS       AR366780               1195 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 1 from patent US 6329503.
ACCESSION   AR366780
VERSION     AR366780.1  GI:34599746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE     Serpentine transmembrane antigens expressed in human cancers and
            uses thereof
  JOURNAL   Patent: US 6329503-A 1 11-DEC-2001;
            Agensys, Inc.; Santa Monica, CA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
```

```
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 3
AR405830
LOCUS       AR405830                1195 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 878 from patent US 6630305.
ACCESSION   AR405830
VERSION     AR405830.1  GI:40154667
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6630305-A 878 07-OCT-2003;
            Corixa Corporation; Seattle, WA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 4
AR564210
LOCUS       AR564210                1195 bp    DNA     linear   PAT 08-OCT-2004
```

```
DEFINITION  Sequence 878 from patent US 6759515.
ACCESSION   AR564210
VERSION     AR564210.1  GI:53979261
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6759515-A 878 06-JUL-2004;
            Corixa Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 5
AR589196
LOCUS       AR589196               1195 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 878 from patent US 6800746.
ACCESSION   AR589196
VERSION     AR589196.1  GI:56636093
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6800746-A 878 05-OCT-2004;
            Corixa Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195

RESULT 6
AR654075

LOCUS       AR654075               1195 bp    DNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 1 from patent US 6887975.
ACCESSION   AR654075
VERSION     AR654075.1  GI:67584962
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE     Peptides derived from STEAP1
  JOURNAL   Patent: US 6887975-A 1 03-MAY-2005;
            Agensys, Inc.; Santa Monica, CA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
```

```
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 7
AX201105
LOCUS       AX201105                1195 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 735 from Patent WO0151633.
ACCESSION   AX201105
VERSION     AX201105.1  GI:15390890
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
            Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0151633-A 735 19-JUL-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy          61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy         121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy         181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy         241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy         301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy         361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy         421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy         481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy         541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy         601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy         661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy         721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy         781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy         841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy         901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy         961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy        1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy        1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy        1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 8
AX267904
```

```
LOCUS       AX267904               1195 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 878 from Patent WO0173032.
ACCESSION   AX267904
VERSION     AX267904.1  GI:16516522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
            and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0173032-A 878 04-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 9
AX926483
LOCUS       AX926483               1195 bp    DNA     linear   PAT 19-DEC-2003
DEFINITION  Sequence 35 from Patent EP1355150.
ACCESSION   AX926483
VERSION     AX926483.1  GI:40246089
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wang,Y.
  TITLE     Panel of nucleic acid sequences for cancer diagnosis
  JOURNAL   Patent: EP 1355150-A 35 22-OCT-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
```

```
Qy       121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy       181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy       241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy       301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy       361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy       421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy       541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy       661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy       721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy       781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy       841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy       901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy       961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy      1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy      1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 10
AX951736
LOCUS       AX951736               1195 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 35 from Patent EP1367138.
ACCESSION   AX951736
VERSION     AX951736.1  GI:40782084
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wang,Y.
  TITLE     Markers for breast cancer prognosis
  JOURNAL   Patent: EP 1367138-A 35 03-DEC-2003;
            Ortho Clinical Diagnostics Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
```

```
Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 11
AX960014
LOCUS       AX960014                1195 bp    DNA     linear   PAT 14-JAN-2004
DEFINITION  Sequence 35 from Patent EP1349104.
ACCESSION   AX960014
VERSION     AX960014.1  GI:40880240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jatkoe,T.
  TITLE     Method of selecting a portfolio of markers for use in a diagnostic
            application
  JOURNAL   Patent: EP 1349104-A 35 01-OCT-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 12
AF186249
LOCUS       AF186249                1195 bp    mRNA    linear   PRI 14-DEC-1999
DEFINITION  Homo sapiens six transmembrane epithelial antigen of prostate
            (STEAP1) mRNA, complete cds.
ACCESSION   AF186249
VERSION     AF186249.1  GI:6572947
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
            Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
            Jakobovits,A., Saffran,D.C. and Afar,D.E.
  TITLE     STEAP: a prostate-specific cell-surface antigen highly expressed in
            human prostate tumors
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)
   PUBMED   10588738
REFERENCE   2  (bases 1 to 1195)
  AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
            Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
            Jakobovits,A., Saffran,D.C. and Afar,D.E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1999) UroGenesys Inc., 1701 Colorado Ave., Santa
            Monica, CA 90404, USA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="7"
                     /map="7p22.3"
     gene            1. .1195
                     /gene="STEAP1"
     CDS             66. .1085
                     /gene="STEAP1"
                     /note="cell surface protein"
                     /codon_start=1
                     /product="six transmembrane epithelial antigen of
                     prostate"
                     /protein_id="AAF17479.1"
                     /db_xref="GI:6572948"
                     /translation="MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLL
                     HLHQTAHADEFDCPSELQHTQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSH
                     QQYFYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLT
                     RKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                     YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
                     WIDIKQFVWYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTE
                     ICSQL"
ORIGIN

  Query Match           100.0%;  Score 1195;  DB 8;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 5.5e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 13
CQ981397
LOCUS       CQ981397                1330 bp    DNA     linear   PAT 25-JAN-2005
DEFINITION  Sequence 252 from Patent EP1498424.
ACCESSION   CQ981397
VERSION     CQ981397.1  GI:58190687
```

```
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Rosenthal,A., Hermann,K., Heiden,E., Pilarsky,C., Bruemmendorf,T.,
            Staub,E., Roepcke,S., Mennerich,D., Kinnemann,H. and Li,X.
  TITLE     Human nucleic acid sequences from lung tumours
  JOURNAL   Patent: EP 1498424-A 252 19-JAN-2005;
            Hinzmann, Bernd (DE); Hermann, Klaus (DE); Heiden, Esmeralda (DE);
            Rosenthal, Andre (DE)
FEATURES             Location/Qualifiers
     source          1. .1330
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1330;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 195

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 255

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 315

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 375

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 435

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 495

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 555

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 615

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 675

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 735

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 795

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 855

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 915

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 975

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 1035

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 1095

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1155

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1215

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1275

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1330


RESULT 14
CS031875
LOCUS       CS031875               1330 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 1381 from Patent WO2005016962.
ACCESSION   CS031875
VERSION     CS031875.1  GI:60731699
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005016962-A 1381 24-FEB-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1330
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1330;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 195

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 255

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 315
```

```
Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 375

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 435

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 495

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 555

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 615

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 675

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 735

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 795

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 855

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 915

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 975

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 1035

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 1095

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1155

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1215

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1275

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1330

RESULT 15
CS036259
LOCUS       CS036259                1330 bp    DNA     linear   PAT 10-MAR-2005
DEFINITION  Sequence 5765 from Patent WO2005016962.
ACCESSION   CS036259
VERSION     CS036259.1  GI:60733938
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Abbas,A., Clark,H., Ouyang,W., Williams,M.P., Wood,W.I. and Wu,T.D.
  TITLE     Compositions and methods for the treatment of immune related
            diseases
  JOURNAL   Patent: WO 2005016962-A 5765 24-FEB-2005;
            Genentech, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1330
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 1195;  DB 6;  Length 1330;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-238;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 195

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 255

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 315

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 375

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 435

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 495

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 555

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 615

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 675

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 735

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        736 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 795

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        796 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 855
```

```
Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        856 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 915

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 975

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        976 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 1035

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1036 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 1095

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1096 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1155

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1156 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1215

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1275

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA 1330
```

Search completed: December 5, 2005, 00:23:41
Job time : 6322.97 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 03:12:22 ; Search time 376.544 Seconds
(without alignments)
987.688 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactcacggtcaagct.....ggaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	40	3.3	1687	6	US-10-750-185-59979	Sequence 59979, A
	2	39.2	3.3	1779	6	US-10-750-185-25365	Sequence 25365, A
c	3	39	3.3	2464	6	US-10-750-185-39315	Sequence 39315, A
	4	38.6	3.2	2133	6	US-10-750-185-26044	Sequence 26044, A
c	5	38.6	3.2	319608	7	US-11-145-703-1	Sequence 1, Appli
c	6	37.6	3.1	1301	6	US-10-750-185-36894	Sequence 36894, A
	7	37.4	3.1	1443	6	US-10-750-185-57750	Sequence 57750, A
c	8	37	3.1	1495	6	US-10-750-185-32077	Sequence 32077, A
	9	37	3.1	1798	6	US-10-750-185-51935	Sequence 51935, A
	10	36.8	3.1	1835	6	US-10-750-185-46765	Sequence 46765, A
c	11	36.8	3.1	2081	6	US-10-750-185-51383	Sequence 51383, A
c	12	36.6	3.1	1620	6	US-10-750-185-52737	Sequence 52737, A
	13	36.4	3.0	2948	7	US-11-099-691-22	Sequence 22, Appl
	14	36.2	3.0	1577	6	US-10-750-185-45671	Sequence 45671, A
c	15	36.2	3.0	1978	6	US-10-750-185-42808	Sequence 42808, A
	16	36.2	3.0	2120	6	US-10-689-742-163	Sequence 163, App
c	17	36.2	3.0	2787	6	US-10-750-185-25062	Sequence 25062, A
c	18	36.2	3.0	3334	6	US-10-821-234-152	Sequence 152, App
	19	36	3.0	872	6	US-10-750-185-49060	Sequence 49060, A
	20	36	3.0	2126	6	US-10-909-125-809	Sequence 809, App
	21	35.8	3.0	1458	6	US-10-821-234-142	Sequence 142, App
c	22	35.8	3.0	2509	6	US-10-750-185-27479	Sequence 27479, A
	23	35.6	3.0	1751	6	US-10-750-185-35358	Sequence 35358, A
	24	35.4	3.0	1646	6	US-10-750-185-41075	Sequence 41075, A
	25	35.2	2.9	894	6	US-10-689-742-5	Sequence 5, Appli
	26	35.2	2.9	925	6	US-10-750-185-46490	Sequence 46490, A
c	27	35.2	2.9	1076	6	US-10-750-185-44612	Sequence 44612, A
	28	35.2	2.9	1328	6	US-10-750-185-42494	Sequence 42494, A
	29	35.2	2.9	1694	6	US-10-689-742-49	Sequence 49, Appl
c	30	35	2.9	399	7	US-11-108-172-547	Sequence 547, App
	31	35	2.9	1034	6	US-10-750-185-61634	Sequence 61634, A
c	32	35	2.9	2508	6	US-10-750-185-40261	Sequence 40261, A
	33	34.8	2.9	1673	6	US-10-750-185-51951	Sequence 51951, A
	34	34.6	2.9	1021	6	US-10-750-185-30480	Sequence 30480, A
	35	34.6	2.9	1407	6	US-10-632-150-5	Sequence 5, Appli
	36	34.6	2.9	1407	7	US-11-073-457-5	Sequence 5, Appli
	37	34.6	2.9	1417	6	US-10-750-185-52014	Sequence 52014, A
c	38	34.4	2.9	2580	6	US-10-750-185-57482	Sequence 57482, A
	39	34.4	2.9	149419	7	US-11-112-908-49	Sequence 49, Appl
	40	34.4	2.9	166111	7	US-11-112-908-47	Sequence 47, Appl
c	41	34.4	2.9	170189	7	US-11-112-908-50	Sequence 50, Appl
	42	34.2	2.9	1012	6	US-10-750-185-54610	Sequence 54610, A
c	43	34.2	2.9	1974	6	US-10-750-185-63164	Sequence 63164, A
	44	34.2	2.9	2906	6	US-10-131-826A-367	Sequence 367, App
c	45	34.2	2.9	3069	6	US-10-750-185-40313	Sequence 40313, A

ALIGNMENTS

RESULT 1
US-10-750-185-59979/c
; Sequence 59979, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59979
; LENGTH: 1687
; TYPE: DNA
; ORGANISM: Bovine 19866880802008
US-10-750-185-59979

Query Match 3.3%; Score 40; DB 6; Length 1687;
Best Local Similarity 55.9%; Pred. No. 1.3;
Matches 76; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

```
Qy       1060 AAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTG 1119
              ||  | |   || ||  |  || ||  |||| |  || || | |||||   | | | ||
Db        507 AACATTAATAATTTTATCTTTTATAATATTATTAGTTTCAAAAATTTTGTCTATAAAATG 448

Qy       1120 ATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAA 1179
                |  ||| | | ||     ||| |  | |  |||||  ||| ||   || | |||  |
Db        447 TTTCATTGTTTGACATTTGTTTTATTTGTTGTTTTGTTTTTAATATTTATACTGAAGAGA 388

Qy       1180 AAAAAAAAAAAAAAAA 1195
                |  ||| | |||| ||
Db        387 AGGAAAGAGAAAAGAA 372
```

RESULT 2
US-10-750-185-25365
; Sequence 25365, Application US/10750185

```
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 25365
;   LENGTH: 1779
;   TYPE: DNA
;   ORGANISM: Bovine  19866880604913
US-10-750-185-25365

  Query Match             3.3%;  Score 39.2;  DB 6;  Length 1779;
  Best Local Similarity   54.1%;  Pred. No. 2.1;
  Matches   80;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        769 TGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGA 828
              ||||||  ||||  ||||| | ||    | | || || | |  ||| | |||||    |
Db        765 TGACATTAATTCTGTCTGTTACTGTTATTCTTACTTGTATCGGGTTTAATTATATCATTA 824

Qy        829 GCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGA 888
                ||||     |   ||   ||| | ||| ||| |  | |   | ||||||  | | | |
Db        825 AAAAGCACATGACACTTAGTCTTTTGCTGTGCAAATAAGATAAAATGATTTGTCCTTTGT 884

Qy        889 ATAAGTGGATAGATATAAAACAATTTGT 916
                |  |  ||    | |||  |  ||||
Db        885 TAACTTATATTTTAAAAAACAATGTTGT 912


RESULT 3
US-10-750-185-39315/c
; Sequence 39315, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 39315
;   LENGTH: 2464
;   TYPE: DNA
;   ORGANISM: Bovine  19866881564211
US-10-750-185-39315

  Query Match             3.3%;  Score 39;  DB 6;  Length 2464;
  Best Local Similarity   50.3%;  Pred. No. 2.7;
  Matches   96;  Conservative    0;  Mismatches   95;  Indels    0;  Gaps    0;

Qy        899 AGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC 958
              ||| | |    || || |    |||| |   |||   |  |  ||| |||   ||
Db       1748 AGAGAAAGGGAAAATTCTGGAATATAAAATGCCATTCTGCAGTATATCTGCAGTCTCAAT 1689

Qy        959 AATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACT 1018
              ||  |    | ||| ||||      | | ||  ||||   |    | | |||||| | |
Db       1688 AACAGCAAGCATGAAATTTGTTCTCTTCCTTGTCCTATTAATAGTTAAGAAGAACAAAGA 1629

Qy       1019 GAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCA 1078
              |||||   | | |   |  |||| ||| |||| |  || |   | || | ||||
Db       1628 CAAGATGTTAAACGTGGGTAAAGAAATCATTAAAAAAACAAACAAACACATGTTTTCCTT 1569

Qy       1079 GTTGTAGAATT 1089
                |  || | ||
Db       1568 CTATTACAGTT 1558


RESULT 4
US-10-750-185-26044
; Sequence 26044, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 26044
;   LENGTH: 2133
;   TYPE: DNA
;   ORGANISM: Bovine  19866880786954
US-10-750-185-26044

  Query Match             3.2%;  Score 38.6;  DB 6;  Length 2133;
  Best Local Similarity   47.0%;  Pred. No. 3.2;
  Matches  119;  Conservative    0;  Mismatches  134;  Indels    0;  Gaps    0;

Qy        915 GTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATA 974
              ||||   || ||  |    |      ||  | | ||| || |||     |    |    | |
Db        762 GTATTTAATTCAATTTTTAAAAGCATATTTGTTGTCTTGCTTTATTATAAAATTAACAAA 821

Qy        975 TTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGT 1034
              | | |     | | || ||  ||     ||     |  |||  |||  ||   |||  |
Db        822 TGCACATAATAAATTTTTCTAACAATACAGAAATGTATAATATAGAAAGTTCCCCATCAT 881

Qy       1035 TGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGT 1094
                | |   ||  |   |  | ||||| || || |  ||  | ||  |||| ||
Db        882 ATAACATAATCCAGAAGTGTATATAAAACAGAAATTTCCTCATAATTCAAGAAATAACTG 941

Qy       1095 TTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTT 1154
              ||    | | ||| ||| |   ||   || |||| |   ||   ||| | | |  || |
Db        942 TTCTTAAAAATTTGGTTTATATTTTCCATTTTTTCTATGCATATTTTAACATATAAATAT 1001

Qy       1155 GTTAATAAAATGA 1167
              || | ||  |||
Db       1002 GTAATTACTTTGA 1014


RESULT 5
US-11-145-703-1/c
; Sequence 1, Application US/11145703
; Publication No. US20050260667A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
```

; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: 53.US16.DIV
; CURRENT APPLICATION NUMBER: US/11/145,703
; CURRENT FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US/10/147,603
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: 09/539,333
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 234
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 319608
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 31..1107
; OTHER INFORMATION: 5'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1108..1289
; OTHER INFORMATION: exon A g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14877..14920
; OTHER INFORMATION: exon B g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 18778..18862
; OTHER INFORMATION: exon Bbis g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 25593..25740
; OTHER INFORMATION: exon C g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29388..29502
; OTHER INFORMATION: exon D g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 29967..30282
; OTHER INFORMATION: exon E g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 64666..64812
; OTHER INFORMATION: exon F g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 65505..65853
; OTHER INFORMATION: exon G g35018 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 65854..67854
; OTHER INFORMATION: 3'regulatory region g35018 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 94124..94964
; OTHER INFORMATION: exon g35017
; FEATURE:
; NAME/KEY: exon
; LOCATION: 201188..201234
; OTHER INFORMATION: exon S g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 214676..214793
; OTHER INFORMATION: exon T g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215702..215746
; OTHER INFORMATION: exon U g35030 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216836..216915
; OTHER INFORMATION: exon V g35030 gene
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 213818..215818
; OTHER INFORMATION: 3'regulatory region g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215941
; OTHER INFORMATION: exon R complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 215819..215975
; OTHER INFORMATION: exon Rbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..216952
; OTHER INFORMATION: exon Qbis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 216661..217061
; OTHER INFORMATION: exon Q complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 217027..217061
; OTHER INFORMATION: exon Q1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 229647..229742
; OTHER INFORMATION: exon X complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 230408..230721
; OTHER INFORMATION: exon P complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231272..231412
; OTHER INFORMATION: exon Obis complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231787..231880
; OTHER INFORMATION: exon O2 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 231870..231879
; OTHER INFORMATION: exon O1 complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 234174..234321
; OTHER INFORMATION: exon O complement g34872 gene
; FEATURE:
; NAME/KEY: exon
; LOCATION: 237406..237428
; OTHER INFORMATION: exon Nbis complement g34872 gene

```
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 239719..239807
;   OTHER INFORMATION: exon N2 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 239719..239853
;   OTHER INFORMATION: exon N complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240528..240569
;   OTHER INFORMATION: exon M1117 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240528..240596
;   OTHER INFORMATION: exon M1090 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240528..240617
;   OTHER INFORMATION: exon M1069 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240528..240644
;   OTHER INFORMATION: exon MS2 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240528..240824
;   OTHER INFORMATION: exon M862 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240528..240994
;   OTHER INFORMATION: exon M692 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240528..241685
;   OTHER INFORMATION: exon M1 complement g34872 gene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 240800..240993
;   OTHER INFORMATION: exon MS1 complement g34872 gene
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 241686..243685
;   OTHER INFORMATION: 5'regulatory region g34872 gene
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 290652..292652
;   OTHER INFORMATION: 3'regulatory region g34665 gene

  Query Match             3.2%;  Score 38.6;  DB 7;  Length 319608;
  Best Local Similarity   48.1%;  Pred. No. 25;
  Matches  139;  Conservative    0;  Mismatches  149;  Indels    1;  Gaps    1;

Qy        905 AAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGT 964
              ||| ||| |  |||| | |             ||||||  |||   |||    ||  ||||
Db      13082 AAACCAACTGTTATGTTTTCTTTTCAGTGAGTTTATGGTAGTCTTTTAAAATCACATTGG 13023

Qy        965 TGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGAT 1024
              ||     || | |  |   |||| || | |   ||   | |   |  | ||| |  | ||
Db      13022 TGGAAATATGTATGTATATATACAATACATCATATATATAATACATTATATATTATATAT 12963

Qy       1025 TAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTA 1084
               |   ||  |     | |  | |   |   ||   ||| |   |||| |      ||  ||
Db      12962 AAATTATAATATATTATATATTATGTATTATATATAAATTATAATATATATTATGTATTA 12903

Qy       1085 GAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAA 1144
               |  ||   | || | | ||| |   | |    | | |||||||||  |   |||
Db      12902 TATATAAATTATA-ATATATTATAAATTATATATTACATATTTTATAATATACACAATTT 12844

Qy       1145 GTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAA 1193
               | | |||   || |||||  |   || | |   | || | ||  | |||
Db      12843 TTATATATAATTTTATAAATTATATAATTATATATAATATAATTATAAA 12795
```

```
RESULT 6
US-10-750-185-36894/c
; Sequence 36894, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36894
;   LENGTH: 1301
;   TYPE: DNA
;   ORGANISM: Bovine  19866881016886
US-10-750-185-36894

  Query Match             3.1%;  Score 37.6;  DB 6;  Length 1301;
  Best Local Similarity   61.0%;  Pred. No. 4.6;
  Matches   61;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy       1096 TACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTG 1155
              | || |||||||  |||   |    | | |||| |    ||   | |||| |||| ||
Db        851 TGCAGACATTTTAATTCTCCAAAATTGTGTTTTGTGTTTAATTCTCCAAGATTGTGTTCT 792

Qy       1156 TTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              |      || |  || |||  | ||||||||||||||||
Db        791 TGTTCTGAAGGTATAATCACAGCAAAAAAAAAAAAAAAAA 752


RESULT 7
US-10-750-185-57750
; Sequence 57750, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 57750
;   LENGTH: 1443
;   TYPE: DNA
;   ORGANISM: Bovine  19866881229395
US-10-750-185-57750

  Query Match             3.1%;  Score 37.4;  DB 6;  Length 1443;
  Best Local Similarity   48.4%;  Pred. No. 5.3;
  Matches  104;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy        980 AAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGA 1039
              || |  | | | | || ||         ||  |||| | ||  ||  | ||||     |||
Db         50 AACCTAAGTGTCCATGACAGATGAACAGATAAAGAAAATGTGGAAAACACATACAATGGA 109
```

```
Qy       1040 AGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACA 1099
              | |    | |||   ||||    ||  |||||||   |      |  ||   ||   |||
Db        110 ATAGTGTAAGAAAGAAAACAGTCTTGTCATATGTTATAACACAGATTATCCTTGAGGACA 169

Qy       1100 CACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAA 1159
              ||    |  ||  ||||    ||     |    |||  | | ||   | |   |  ||
Db        170 CAATGCTAAGTCAAATAAGCCAATCACAAAAAGGCAAACTCTGAATGATTTCACTTGTAT 229

Qy       1160 TAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAA 1194
              ||||    | || |||  |||  ||| ||| | ||
Db        230 TAAATATCTAATACAATCAAACCAAAGAAACAGAA 264


RESULT 8
US-10-750-185-32077/c
; Sequence 32077, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 32077
;   LENGTH: 1495
;   TYPE: DNA
;   ORGANISM: Bovine  19866881171280
US-10-750-185-32077

  Query Match             3.1%;  Score 37;  DB 6;  Length 1495;
  Best Local Similarity   53.0%;  Pred. No. 6.8;
  Matches   79;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy       1046 CACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACATT 1105
              |||  ||||||   |   |  |   | ||    ||  || ||| ||||||   |   |
Db       1068 CACTAAAATTTGAATTTCGTATCATTTTTAAGTGTCCTAAAATAACTGTTCTTAATTAAA 1009

Qy       1106 TTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAAAT 1165
              ||  |||||    |   | | |   | | |    | | ||||   |||   | |||||||
Db       1008 TTATTTCAACCATTTAAAAATGCAAAATCTTTCTGTAAAGTAATTATCCTTCAATAAAAA 949

Qy       1166 GATTATTCAAGGAAAAAAAAAAAAAAAAA 1194
                 || ||    |||| ||||||| ||||
Db        948 ATAAATGCATTTTAAAACAAAAAATAAAA 920


RESULT 9
US-10-750-185-51935
; Sequence 51935, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51935
;   LENGTH: 1798
;   TYPE: DNA
;   ORGANISM: Bovine  19866880871433
US-10-750-185-51935

  Query Match             3.1%;  Score 37;  DB 6;  Length 1798;
  Best Local Similarity   62.4%;  Pred. No. 7.3;
  Matches   58;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy       1102 CATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATA 1161
              ||||||   || |  |  || || ||||| |  ||| | |||| |   ||  | || ||
Db        155 CATTTTATCTCTAAGTCAATTTAATTTATAAGGAACGTATCAAATAAATAGCTCTTGATT 214

Qy       1162 AAATGATTATTCAAGGAAAAAAAAAAAAAAAAA 1194
                 ||  || || | |||| | ||||| || |||
Db        215 CTATATTTCTTTATGGAAGAGAAAAAGAACAAA 247


RESULT 10
US-10-750-185-46765
; Sequence 46765, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 46765
;   LENGTH: 1835
;   TYPE: DNA
;   ORGANISM: Bovine  19866880952210
US-10-750-185-46765

  Query Match             3.1%;  Score 36.8;  DB 6;  Length 1835;
  Best Local Similarity   52.6%;  Pred. No. 8.2;
  Matches   80;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy       1044 GTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACA 1103
              |||   |  ||||| | |     | | |  |   ||||        ||| || ||||
Db       1322 GTCTTTATTATTAAAATATGAATGTTGTTGTTGTAGTTACTATGCAACTCTTGACACTGC 1381

Qy       1104 TTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAA 1163
                |  | |||||||  | ||||  | || |  | |  |  | |||   ||| || | |
Db       1382 CAAATAATTAATATTGTAAAATTTACTGACTAGAAATATATATATGTGGGTGTAAACATA 1441

Qy       1164 ATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              |  ||  | |  ||||||    |||||| |||
Db       1442 AATATATTACTGGGAAAAGGTTAAAAAATAAA 1473


RESULT 11
US-10-750-185-51383/c
; Sequence 51383, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
```

```
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 51383
;   LENGTH: 2081
;   TYPE: DNA
;   ORGANISM: Bovine  19866880958299
US-10-750-185-51383

  Query Match             3.1%;  Score 36.8;  DB 6;  Length 2081;
  Best Local Similarity   58.0%;  Pred. No. 8.7;
  Matches   65;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy       1084 AGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCA 1143
             | ||| | |||| |      ||  |  |||||  |||||||   ||||      | ||   |
Db        472 AAAATCAGTGTTGATTATGATAATCATTCAAATTTGATATTCCTTATTTATTATATACAA 413

Qy       1144 AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
             | || | | |   | | |  | ||    |   ||||||||||||||||| ||
Db        412 ATTTAGAAATAAATCACATTAGGAAAGATTTTGGAAAAAAAAAAAAAAACAA 361


RESULT 12
US-10-750-185-52737/c
; Sequence 52737, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 52737
;   LENGTH: 1620
;   TYPE: DNA
;   ORGANISM: Bovine  19866881330166
US-10-750-185-52737

  Query Match             3.1%;  Score 36.6;  DB 6;  Length 1620;
  Best Local Similarity   57.4%;  Pred. No. 8.7;
  Matches   66;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy       1080 TTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACAT 1139
             || ||| |  | | ||| |    |||||| |  ||  | ||  ||||||||     | |
Db        345 TTATAGCAAAATTATTTTCCAGTATTTTTTTAAAAACTAGAGCTATTTTATAGGGGATAC 286

Qy       1140 TTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1194
             || |||   ||||||     | ||||||   |   |      | | ||||||||||
Db        285 TTGAAGCCAGTATTTAAGCTTTAAATGACAGTAATATTGGCATAGAAAAAAAAAA 231


RESULT 13
US-11-099-691-22
; Sequence 22, Application US/11099691
; Publication No. US20050260644A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE PHARMACEUTICALS, INC.
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  HILLMAN, Jennifer L.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  YUE, Henry
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  PATTERSON, Chandra
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  YANG, Junming
;  TITLE OF INVENTION: CELL SIGNALING PROTEINS
;  FILE REFERENCE: PF-0521 PCT
;  CURRENT APPLICATION NUMBER: US/11/099,691
;  CURRENT FILING DATE:  2005-04-06
;  PRIOR APPLICATION NUMBER: US/09/700,444
;  PRIOR FILING DATE: 2002-08-26
;  PRIOR APPLICATION NUMBER: 60/085,343
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/098,010
;  PRIOR FILING DATE: 1998-08-26
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PERL Program
; SEQ ID NO 22
;   LENGTH: 2948
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc-feature
;   OTHER INFORMATION: Incyte Clone 1403604
US-11-099-691-22

  Query Match             3.0%;  Score 36.4;  DB 7;  Length 2948;
  Best Local Similarity   59.8%;  Pred. No. 13;
  Matches   61;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy       1094 TTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTCAAGTTTGTATT 1153
             |||||  ||||  || || ||| ||    ||||   ||   |    || |  ||| ||
Db       2846 TTTACCAACATACTTTTTAAATGTTTTGCTATTGGTTCCATATTTATTTAGATTTATAAG 2905

Qy       1154 TGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
             ||| ||||||   |   ||  | |    ||||||||||||||
Db       2906 TGTCAATAAAGCAAACTTTTGATGCCTCAAAAAAAAAAAAAA 2947


RESULT 14
US-10-750-185-45671
; Sequence 45671, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 45671
;   LENGTH: 1577
;   TYPE: DNA
;   ORGANISM: Bovine  19866880420845
US-10-750-185-45671

  Query Match             3.0%;  Score 36.2;  DB 6;  Length 1577;
```

Best Local Similarity 50.3%; Pred. No. 11;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

```
Qy       1012 AGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATAT 1071
              ||  ||| |   ||| |  |  |    || |   ||   |     | ||     || ||
Db        922 AGGCACTTATATTTAAAATTTTTGTACAAAAGTACAATTATGACCAAAATTAAAAGGTAA 981

Qy       1072 GTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATC 1131
                 | |  |||| |||    |   | |||    ||     | || ||||||  |
Db        982 ACAAAAAATATTAGAGTTATATGTAGAAAACAAAGGTGGAAGCTCTTTATATATATATAT 1041

Qy       1132 ACCAACATTTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAA 1188
              |   | || |  | ||| ||||  | ||||||||||| ||   || |||||||  |||
Db       1042 ATATATATATATAATTTATATTACTAAATAAAATGAGTACATAAAGAAAAAAGTAAA 1098
```

RESULT 15
US-10-750-185-42808/c
; Sequence 42808, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 42808
; LENGTH: 1978
; TYPE: DNA
; ORGANISM: Bovine 19866880681507
US-10-750-185-42808

Query Match 3.0%; Score 36.2; DB 6; Length 1978;
Best Local Similarity 62.2%; Pred. No. 12;
Matches 74; Conservative 0; Mismatches 43; Indels 2; Gaps 1;

```
Qy       1079 GTTGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGA--TATATTTTATCACCAA 1136
              ||  |  |||  ||| |||     | | ||| || |||||||  || ||||  |    ||
Db       1569 GTATTTAAATCTCTGATTAATTTAAATCTTGCTCTATATTGACTTAAATTTGCTTTGAAA 1510

Qy       1137 CATTTCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              || |     |||  | ||||||| |   | ||| | | || |  ||||||||||||||
Db       1509 CAATAGGGATTTTCAATTGTTAAGAGTCTTATTTTGCCAGAAGCAAAAAAAAAAAAAAA 1451
```

Search completed: December 5, 2005, 08:05:49
Job time : 379.544 secs

This Page Blank (uspto)

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:43:36 ; Search time 238.244 Seconds
(without alignments)
8916.024 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactcacggtcaagct.....ggaaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1195	100.0	1195	3	US-09-323-873A-1	Sequence 1, Appli
	2	1195	100.0	1195	3	US-09-685-166A-878	Sequence 878, App
	3	1195	100.0	1195	3	US-09-679-426-878	Sequence 878, App
	4	1195	100.0	1195	3	US-09-759-143-878	Sequence 878, App
	5	1195	100.0	1195	3	US-10-010-667A-1	Sequence 1, Appli
	6	1195	100.0	1195	3	US-10-012-896-878	Sequence 878, App
	7	1193	99.8	1193	3	US-09-455-486-1	Sequence 1, Appli
	8	1143.4	95.7	1147	3	US-09-949-016-2686	Sequence 2686, Ap
	9	825.6	69.1	3627	3	US-09-323-873A-6	Sequence 6, Appli
	10	825.6	69.1	3627	3	US-09-455-486-4	Sequence 4, Appli
	11	825.6	69.1	3627	3	US-10-010-667A-6	Sequence 6, Appli
c	12	581	48.6	592	3	US-09-439-313-342	Sequence 342, App
c	13	581	48.6	592	3	US-09-352-616A-342	Sequence 342, App
c	14	581	48.6	592	3	US-09-636-215-342	Sequence 342, App
c	15	581	48.6	592	3	US-09-685-166A-342	Sequence 342, App
c	16	581	48.6	592	3	US-09-679-426-342	Sequence 342, App
c	17	581	48.6	592	3	US-09-759-143-342	Sequence 342, App
c	18	581	48.6	592	3	US-09-651-236-342	Sequence 342, App
c	19	581	48.6	592	3	US-09-657-279-342	Sequence 342, App
c	20	581	48.6	592	3	US-10-012-896-342	Sequence 342, App
	21	515.6	43.1	9073	3	US-09-949-016-14428	Sequence 14428, A
	22	360.6	30.2	455	3	US-09-621-976-9264	Sequence 9264, Ap
	23	266.6	22.3	2453	3	US-09-455-486-5	Sequence 5, Appli
	24	266.6	22.3	2469	3	US-10-104-047-1185	Sequence 1185, Ap
	25	265	22.2	1403	3	US-10-012-896-995	Sequence 995, App
c	26	229.6	19.2	848	3	US-10-012-896-993	Sequence 993, App
	27	221.4	18.5	519	3	US-10-010-667A-7	Sequence 7, Appli
	28	221.4	18.5	521	3	US-09-323-873A-7	Sequence 7, Appli
	29	212.8	17.8	2714	3	US-09-562-930-5	Sequence 5, Appli
	30	212.8	17.8	3884	3	US-09-562-930-10	Sequence 10, Appl
	31	187.4	15.7	4429	3	US-09-455-486-7	Sequence 7, Appli
	32	184.8	15.5	1213	3	US-09-083-521-3	Sequence 3, Appli
	33	171	14.3	1886	3	US-09-562-930-1	Sequence 1, Appli
c	34	166.6	13.9	1203	3	US-09-544-618-6	Sequence 6, Appli
c	35	162.4	13.6	366	3	US-09-030-607-215	Sequence 215, App
c	36	162.4	13.6	366	3	US-09-439-313-215	Sequence 215, App
c	37	162.4	13.6	366	3	US-09-352-616A-215	Sequence 215, App
c	38	162.4	13.6	366	3	US-09-232-149A-215	Sequence 215, App
c	39	162.4	13.6	366	3	US-09-159-812-215	Sequence 215, App
c	40	162.4	13.6	366	3	US-09-636-215-215	Sequence 215, App
c	41	162.4	13.6	366	3	US-09-685-166A-215	Sequence 215, App
c	42	162.4	13.6	366	3	US-09-115-453-215	Sequence 215, App
c	43	162.4	13.6	366	3	US-09-688-489-215	Sequence 215, App
c	44	162.4	13.6	366	3	US-09-679-426-215	Sequence 215, App
c	45	162.4	13.6	366	3	US-09-759-143-215	Sequence 215, App

ALIGNMENTS

RESULT 1
US-09-323-873A-1
; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-1

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6.6e-301;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
```

```
Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 2
US-09-685-166A-878
; Sequence 878, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-685-166A-878

  Query Match             100.0%;  Score 1195;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-301;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

RESULT 3
US-09-679-426-878
; Sequence 878, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens

US-09-679-426-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 6.6e-301;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
```

```
Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 4
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-759-143-878

  Query Match             100.0%;  Score 1195;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-301;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 5
US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Hubert, Rene S.
;  APPLICANT:  Leong, Kahan
;  APPLICANT:  Raitano, Arthur B.
;  APPLICANT:  Saffran, Douglas C.
;  APPLICANT:  Mitchell, Steve Chappell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
```

```
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001601
;  CURRENT APPLICATION NUMBER: US/10/010,667A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-10-010-667A-1

  Query Match             100.0%;  Score 1195;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 6.6e-301;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 6
US-10-012-896-878
; Sequence 878, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Wantanabe, Yoshihiro
;  APPLICANT:  Meagher, Madeleine Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C27
;  CURRENT APPLICATION NUMBER: US/10/012,896
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 1011
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-896-878

  Query Match             100.0%;  Score 1195;  DB 3;  Length 1195;
```

```
  Best Local Similarity   100.0%;  Pred. No. 6.6e-301;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 7
US-09-455-486-1
; Sequence 1, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
;  APPLICANT:  Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION:  NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE:  129.17-US-I1
;  CURRENT APPLICATION NUMBER: US/09/455,486
;  CURRENT FILING DATE:  1999-12-06
;  PRIOR APPLICATION NUMBER:  09/323,873
;  PRIOR FILING DATE:  1999-06-01
;  NUMBER OF SEQ ID NOS:  34
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-09-455-486-1

  Query Match             99.8%;  Score 1193;  DB 3;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-300;
  Matches 1193;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           3 GAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAGAA 62
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAGAA 60

Qy          63 TTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG 122
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 TTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG 120

Qy         123 AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAA 182
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAA 180

Qy         183 AGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA 242
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 AGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCA 240

Qy         243 GAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCT 302
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 GAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCT 300

Qy         303 ATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCA 362
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCA 360

Qy         363 ACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCA 422
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 ACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCA 420

Qy         423 ATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTC 482
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        421 ATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTC 480

Qy        483 CAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTA 542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTA 540

Qy        543 ACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGT 602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 ACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGT 600

Qy        603 CTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAG 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAG 660

Qy        663 GTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTAT 722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTAT 720

Qy        723 GTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCA 782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCA 780

Qy        783 TCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATT 842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATT 840

Qy        843 GTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGAT 902
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGAT 900

Qy        903 ATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATT 962
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATT 960

Qy        963 GTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAG 1022
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAG 1020

Qy       1023 ATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080

Qy       1083 TAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTC 1142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATTTC 1140

Qy       1143 AAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 AAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1193
```

```
RESULT 8
US-09-949-016-2686
; Sequence 2686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2686
;   LENGTH: 1147
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2686

  Query Match             95.7%;  Score 1143.4;  DB 3;  Length 1147;
  Best Local Similarity   99.9%;  Pred. No. 1.7e-287;
  Matches 1144;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         34 GGTGGCTGAAGCCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACC 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGTGGCTGAAGCCATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACC 60

Qy         94 AAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATA 153
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGAAGACGATTATTTGCATA 120

Qy        154 AGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCACCAAACAG 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        121 AGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCAGCAAACAG 180

Qy        214 CCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCAC 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTTCCAC 240

Qy        274 AGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTC 333
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTC 300

Qy        334 TTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTC 393
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAAATTC 360

Qy        394 CAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTT 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTGGTTT 420

Qy        454 ACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGT 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGT 480

Qy        514 TTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCT 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCT 540

Qy        574 TTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGAT 633
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGAT 600

Qy        634 ACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTG 693
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTG 660

Qy        694 AGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATAC 753
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATAC 720

Qy        754 TGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAAT 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAAT 780

Qy        814 TTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCAT 873
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 TTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCAT 840

Qy        874 TGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAA 933
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAA 900

Qy        934 CTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCC 993
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 CTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCC 960

Qy        994 TGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAA 1053
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        961 TGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAA 1020

Qy       1054 TTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCA 1113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 TTAACAAAACTGAGATATGTTCCCAGTTGTAGAATTACTGTTTACACACATTTTTGTTCA 1080

Qy       1114 ATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAAATGATTATTC 1173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATATTGATATATTTTATCACCAACATTTCAAGTTTGTATTTGTTAATAAAATGATTATTC 1140

Qy       1174 AAGGA 1178
              |||||
Db       1141 AAGGA 1145
```

RESULT 9
US-09-323-873A-6
; Sequence 6, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-6

Query Match 69.1%; Score 825.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-204;
Matches 828; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 90

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 150

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 210

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 270

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 330

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        331 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAG 390

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 450

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 510

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 570

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 630

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 690

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 750

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 810

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAA 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||    ||
Db        811 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGTAAA 862
```

RESULT 10
US-09-455-486-4
; Sequence 4, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-I1
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-486-4

Query Match 69.1%; Score 825.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-204;
Matches 828; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 90

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 150

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 210

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
```

```
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 270

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 330

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        331 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAG 390

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 450

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 510

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 570

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 630

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 690

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 750

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 810

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAA 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        811 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGTAAA 862
```

RESULT 11
US-10-010-667A-6
; Sequence 6, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-667A-6

```
  Query Match             69.1%;  Score 825.6;  DB 3;  Length 3627;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-204;
  Matches  828;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 90

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 150

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 210

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 270

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 330

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        331 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAG 390

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 450

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 510

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 570

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 630

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 690

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 750

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 810

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAA 832
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Db        811 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGTAAA 862
```

RESULT 12
US-09-439-313-342/c
; Sequence 342, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.

```
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;    LENGTH: 592
;    TYPE: DNA
;    ORGANISM: Homo sapien
US-09-439-313-342

  Query Match             48.6%;  Score 581;  DB 3;  Length 592;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-141;
  Matches  581;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 524

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 464

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 404

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 344

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 284

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 224

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 164

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 104

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 44

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 583
              |||||||||||||: |||||||||||||||||||||||||||||
Db         43 TAACAAGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1


RESULT 13
US-09-352-616A-342/c
; Sequence 342, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427C8
;  CURRENT APPLICATION NUMBER: US/09/352,616A
;  CURRENT FILING DATE:  1999-07-13
;  NUMBER OF SEQ ID NOS:  472
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-352-616A-342

  Query Match             48.6%;  Score 581;  DB 3;  Length 592;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-141;
  Matches  581;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 524

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 464

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 404

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 344

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 284

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 224

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 164

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 104

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 44

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 583
              |||||||||||||: |||||||||||||||||||||||||||||
Db         43 TAACAAGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1


RESULT 14
US-09-636-215-342/c
; Sequence 342, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
```

```
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-636-215-342

  Query Match             48.6%;  Score 581;  DB 3;  Length 592;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-141;
  Matches  581;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 524

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 464

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 404

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 344

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 284

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 224

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 164

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 104

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 44

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 583
              |||||||||||||: ||||||||||||||||||||||||||||
Db         43 TAACAAGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1


RESULT 15
US-09-685-166A-342/c
; Sequence 342, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-685-166A-342

  Query Match             48.6%;  Score 581;  DB 3;  Length 592;
  Best Local Similarity   99.7%;  Pred. No. 2.6e-141;
  Matches  581;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        583 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 524

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        523 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 464

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        463 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 404

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        403 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 344

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        343 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 284

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        283 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 224

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 164

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 104

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        103 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 44

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 583
              |||||||||||||: ||||||||||||||||||||||||||||
Db         43 TAACAAGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1


Search completed: December  5, 2005, 03:19:37
```

Job time : 241.244 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 00:23:57 ; Search time 1115.59 Seconds
(without alignments)
8858.046 Million cell updates/sec

Title: US-10-750-262-1
Perfect score: 1195
Sequence: 1 ccgagactcacggtcaagct.....ggaaaaaaaaaaaaaaaaa 1195

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1195	100.0	1195	3	US-09-759-143-878	Sequence 878, App
2	1195	100.0	1195	3	US-09-780-669-878	Sequence 878, App
3	1195	100.0	1195	3	US-09-822-827-878	Sequence 878, App
4	1195	100.0	1195	3	US-09-895-793-878	Sequence 878, App
5	1195	100.0	1195	3	US-09-895-814-878	Sequence 878, App
6	1195	100.0	1195	5	US-10-012-896-878	Sequence 878, App
7	1195	100.0	1195	5	US-10-011-095-1	Sequence 1, Appli
8	1195	100.0	1195	5	US-10-010-667A-1	Sequence 1, Appli
9	1195	100.0	1195	5	US-10-205-823-396	Sequence 396, App
10	1195	100.0	1195	6	US-10-144-678A-878	Sequence 878, App
11	1195	100.0	1195	6	US-10-294-025-878	Sequence 878, App
12	1195	100.0	1195	6	US-10-393-590-35	Sequence 35, Appl
13	1195	100.0	1195	6	US-10-393-567-35	Sequence 35, Appl
14	1195	100.0	1195	6	US-10-394-087-35	Sequence 35, Appl
15	1195	100.0	1195	6	US-10-295-027-713	Sequence 713, App
16	1195	100.0	1195	6	US-10-295-027-1130	Sequence 1130, Ap
17	1195	100.0	1195	8	US-10-643-795A-16	Sequence 16, Appl
18	1195	100.0	1195	8	US-10-643-795A-42	Sequence 42, Appl
19	1195	100.0	1195	9	US-10-750-262-1	Sequence 1, Appli
20	1195	100.0	1195	9	US-10-948-518-16	Sequence 16, Appl
21	1195	100.0	1195	9	US-10-948-518-42	Sequence 42, Appl
22	1195	100.0	1195	9	US-10-956-157-1811	Sequence 1811, Ap
23	1195	100.0	1195	9	US-10-956-157-7046	Sequence 7046, Ap
24	1195	100.0	1195	9	US-10-858-887-1	Sequence 1, Appli
25	1195	100.0	1195	9	US-10-631-467-428	Sequence 428, App
26	1195	100.0	1195	10	US-11-051-454-396	Sequence 396, App
27	1195	100.0	1330	7	US-10-755-889-191	Sequence 191, App
28	1193	99.8	1193	6	US-10-165-044-1	Sequence 1, Appli
29	1193	99.8	1193	7	US-10-408-009-1	Sequence 1, Appli
30	1193	99.8	1193	8	US-10-857-785-1	Sequence 1, Appli
31	1193	99.8	1193	8	US-10-856-109-1	Sequence 1, Appli
32	1193	99.8	1193	8	US-10-753-195-1	Sequence 1, Appli
33	1193	99.8	1193	9	US-10-752-421-1	Sequence 1, Appli
34	1181.8	98.9	1193	8	US-10-830-899-2	Sequence 2, Appli
35	1181.8	98.9	1193	9	US-10-861-662-2	Sequence 2, Appli
36	1178	98.6	1277	3	US-09-814-353-19910	Sequence 19910, A
37	1177	98.5	1177	8	US-10-696-639-15	Sequence 15, Appl
38	1177	98.5	1201	7	US-10-425-114-16445	Sequence 16445, A
39	1166	97.6	1354	8	US-10-723-860-5120	Sequence 5120, Ap
40	1048	87.7	1365	8	US-10-830-899-6	Sequence 6, Appli
41	1048	87.7	1365	9	US-10-861-662-6	Sequence 6, Appli
42	827.2	69.2	3627	8	US-10-830-899-10	Sequence 10, Appl
43	827.2	69.2	3627	9	US-10-861-662-10	Sequence 10, Appl
44	825.6	69.1	3627	5	US-10-011-095-6	Sequence 6, Appli
45	825.6	69.1	3627	5	US-10-010-667A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Query Match 100.0%; Score 1195; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 1.1e-281;
Matches 1195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
```

```
Qy       121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
Db       121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy       181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
Db       181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy       241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
Db       241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy       301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
Db       301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy       361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
Db       361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy       421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
Db       421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
Db       481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy       541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
Db       541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
Db       601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy       661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
Db       661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy       721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
Db       721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy       781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
Db       781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy       841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
Db       841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy       901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
Db       901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy       961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
Db       961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy      1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
Db      1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy      1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
Db      1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
Db      1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 2
US-09-780-669-878
; Sequence 878, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C24
;  CURRENT APPLICATION NUMBER: US/09/780,669
;  CURRENT FILING DATE:  2001-02-09
;  NUMBER OF SEQ ID NOS:  943
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-780-669-878

  Query Match            100.0%;  Score 1195;  DB 3;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
```

```
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 3
US-09-822-827-878
; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.534C1
;  CURRENT APPLICATION NUMBER: US/09/822,827
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 982
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-822-827-878

  Query Match             100.0%;  Score 1195;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
```

```
Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 4
US-09-895-793-878
; Sequence 878, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.534C2
;  CURRENT APPLICATION NUMBER: US/09/895,793
;  CURRENT FILING DATE:  2001-06-29
;  NUMBER OF SEQ ID NOS: 982
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-895-793-878

  Query Match             100.0%;  Score 1195;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 5
US-09-895-814-878
; Sequence 878, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
```

```
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C26
;  CURRENT APPLICATION NUMBER: US/09/895,814
;  CURRENT FILING DATE:  2001-06-29
;  NUMBER OF SEQ ID NOS: 990
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-895-814-878

  Query Match             100.0%;  Score 1195;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 6
US-10-012-896-878
; Sequence 878, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Wantanabe, Yoshihiro
;  APPLICANT:  Meagher, Madeleine Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C27
;  CURRENT APPLICATION NUMBER: US/10/012,896
```

```
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 1011
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;    LENGTH: 1195
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-012-896-878

  Query Match             100.0%;  Score 1195;  DB 5;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 7
US-10-011-095-1
; Sequence 1, Application US/10011095
; Publication No. US20030045682A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Hubert, Rene S.
;  APPLICANT:  Leong, Kahan
;  APPLICANT:  Raitano, Arthur B.
;  APPLICANT:  Saffran, Douglas C.
;  APPLICANT:  Mitchell, Steve Chappell
;  TITLE OF INVENTION: ANTIBODIES IMMUNOSPECIFIC FOR STEAP1 (AS AMENDED)
;  FILE REFERENCE: 511582001610
;  CURRENT APPLICATION NUMBER: US/10/011,095
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;    LENGTH: 1195
;    TYPE: DNA
;    ORGANISM: Homo Sapiens
US-10-011-095-1

  Query Match             100.0%;  Score 1195;  DB 5;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
```

```
Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
```

```
RESULT 8
US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Publication No. US20030055217A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Hubert, Rene S.
;  APPLICANT:  Leong, Kahan
;  APPLICANT:  Raitano, Arthur B.
;  APPLICANT:  Saffran, Douglas C.
;  APPLICANT:  Mitchell, Steve Chappell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001601
;  CURRENT APPLICATION NUMBER: US/10/010,667A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-10-010-667A-1

  Query Match             100.0%;  Score 1195;  DB 5;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 9
US-10-205-823-396
; Sequence 396, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
;  APPLICANT: Schlegel, Robert
;  APPLICANT:  Monahan, John E.
;  APPLICANT:  Endege, Wilson O.
;  APPLICANT:  Gannavarapu, Manjula
;  APPLICANT:  Gorbatcheva, Bella
;  APPLICANT:  Hoersch, Sebastian
;  APPLICANT:  Kamatkar, Shubhangi
;  APPLICANT:  Wonsey, Angela M.
;  APPLICANT:  Glatt, Karen
;  APPLICANT:  Zhao, Xumei
;  APPLICANT:  Anderson, Dustin
;  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;  TITLE OF INVENTION:  METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;  TITLE OF INVENTION:  THERAPY OF PROSTATE CANCER
;  FILE REFERENCE: MRI-044
;  CURRENT APPLICATION NUMBER: US/10/205,823
;  CURRENT FILING DATE:  2002-07-25
;  PRIOR APPLICATION NUMBER: 60/307,982
;  PRIOR FILING DATE: 2001-07-25
;  PRIOR APPLICATION NUMBER: 60/314,356
;  PRIOR FILING DATE: 2001-08-22
;  PRIOR APPLICATION NUMBER: 60/325,020
;  PRIOR FILING DATE: 2001-09-25
;  PRIOR APPLICATION NUMBER: 60/341,746
;  PRIOR FILING DATE: 2001-12-12
;  PRIOR APPLICATION NUMBER: 60/362,158
;  PRIOR FILING DATE: 2002-03-05
;  NUMBER OF SEQ ID NOS: 455
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 396
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-205-823-396

  Query Match             100.0%;  Score 1195;  DB 5;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;

  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
```

```
Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 10
US-10-144-678A-878
; Sequence 878, Application US/10144678A
; Publication No. US20030157089A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A. W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals y de Bassols, Carlota
;  APPLICANT:  Foy, Teresa M.
;  APPLICANT:  Watanabe, Yoshihiro
;  APPLICANT:  Deng, Ta
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C28
;  CURRENT APPLICATION NUMBER: US/10/144,678A
;  CURRENT FILING DATE:  2002-08-12
;  NUMBER OF SEQ ID NOS: 1033
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-144-678A-878

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 11
US-10-294-025-878
; Sequence 878, Application US/10294025
; Publication No. US20030185830A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Kalos, Michael D.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
```

```
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C29
;  CURRENT APPLICATION NUMBER: US/10/294,025
;  CURRENT FILING DATE:  2002-11-12
;  NUMBER OF SEQ ID NOS: 1038
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-294-025-878

  Query Match            100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195


RESULT 12
US-10-393-590-35
; Sequence 35, Application US/10393590
; Publication No. US20030190656A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, YIXIN
;  TITLE OF INVENTION: BREAST CANCER PROGNASTIC PORTFOLIO
;  FILE REFERENCE: CDS 268 US NP
;  CURRENT APPLICATION NUMBER: US/10/393,590
;  CURRENT FILING DATE:  2003-03-21
;  PRIOR APPLICATION NUMBER: 60/368,789
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: human
US-10-393-590-35

  Query Match            100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
```

```
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195

RESULT 13
US-10-393-567-35
; Sequence 35, Application US/10393567
; Publication No. US20030194733A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, YIXIN
;  TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL
;  FILE REFERENCE: CDS 269 US NP
;  CURRENT APPLICATION NUMBER: US/10/393,567
;  CURRENT FILING DATE:  2003-03-21
;  PRIOR APPLICATION NUMBER: 60/368,667
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: human
US-10-393-567-35

  Query Match           100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 14
US-10-394-087-35
; Sequence 35, Application US/10394087
; Publication No. US20030194734A1
; GENERAL INFORMATION:
;  APPLICANT: Jatkoe, Tim
;  TITLE OF INVENTION: SELECTION OF MARKERS
;  FILE REFERENCE: CDS 265 US NP
;  CURRENT APPLICATION NUMBER: US/10/394,087
;  CURRENT FILING DATE:  2003-03-21
;  PRIOR APPLICATION NUMBER: 60/368,790
;  PRIOR FILING DATE: 2002-03-29
;  NUMBER OF SEQ ID NOS: 100
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: human
US-10-394-087-35

  Query Match             100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAA 1195


RESULT 15
US-10-295-027-713
; Sequence 713, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Aziz, Natasha
;  APPLICANT:  Ginsberg, Wendy M.
;  APPLICANT:  Gish, Kurt C.
;  APPLICANT:  Glynne, Richard
;  APPLICANT:  Hevezi, Peter A.
;  APPLICANT:  Mack, David H.
;  APPLICANT:  Murray, Richard
;  APPLICANT:  Watson, Susan R.
;  APPLICANT:  Eos Biotechnology, Inc.
;  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
;  TITLE OF INVENTION:  Methods of Screening for Modulators of Cancer
;  FILE REFERENCE: 018501-012500US
;  CURRENT APPLICATION NUMBER: US/10/295,027
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: US 09/663,733
;  PRIOR FILING DATE: 2000-09-15
;  PRIOR APPLICATION NUMBER: US 60/350,666
;  PRIOR FILING DATE: 2001-11-13
;  PRIOR APPLICATION NUMBER: US 60/335,394
;  PRIOR FILING DATE: 2001-11-15
```

```
;  PRIOR APPLICATION NUMBER: US 60/332,464
;  PRIOR FILING DATE: 2001-11-21
;  PRIOR APPLICATION NUMBER: US 60/334,393
;  PRIOR FILING DATE: 2001-11-29
;  PRIOR APPLICATION NUMBER: US 60/340,376
;  PRIOR FILING DATE: 2001-12-14
;  PRIOR APPLICATION NUMBER: US 60/347,211
;  PRIOR FILING DATE: 2002-01-08
;  PRIOR APPLICATION NUMBER: US 60/347,349
;  PRIOR FILING DATE: 2002-01-10
;  PRIOR APPLICATION NUMBER: US 60/355,250
;  PRIOR FILING DATE: 2002-02-08
;  PRIOR APPLICATION NUMBER: US 60/356,714
;  PRIOR FILING DATE: 2002-02-13
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1386
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 713
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-295-027-713

  Query Match           100.0%;  Score 1195;  DB 6;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-281;
  Matches 1195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCCATACTATTTTATAG 60

Qy         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTA 120

Qy        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAA 180

Qy        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AAAGACCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTT 240

Qy        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAACTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTG 300

Qy        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAG 360

Qy        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGC 420

Qy        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CAATGGTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTG 480

Qy        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGT 540

Qy        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATA 600

Qy        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAAC 660

Qy        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTT 720

Qy        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTC 780

Qy        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA 840

Qy        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAG 900

Qy        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 960

Qy        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGA 1020

Qy       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGT 1080

Qy       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TGTAGAATTACTGTTTACACACATTTTTGTTCAATATTGATATATTTTATCACCAACATT 1140

Qy       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TCAAGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAA 1195

Search completed: December  5, 2005, 07:54:08
Job time : 1120.59 secs
```

This Page Blank (uspto)

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2005, 16:30:04 ; Search time 948 Seconds
(without alignments)
2957.088 Million cell updates/sec

Title: US-10-750-262-2
Perfect score: 1790
Sequence: 1 MESRKDITNQEELWKMKPRR.....IRHGWEDVTKINKTEICSQL 339

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10750262/runat_06122005_162947_15675/app_query.fasta_1.519
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10750262_@CGN_1_1_1026_@runat_06122005_162947_15675
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1790	100.0	1177	8	US-10-696-639-15	Sequence 15, Appl
2	1790	100.0	1193	6	US-10-165-044-1	Sequence 1, Appli
3	1790	100.0	1193	7	US-10-408-009-1	Sequence 1, Appli
4	1790	100.0	1193	8	US-10-857-785-1	Sequence 1, Appli
5	1790	100.0	1193	8	US-10-856-109-1	Sequence 1, Appli
6	1790	100.0	1193	8	US-10-830-899-2	Sequence 2, Appli
7	1790	100.0	1193	8	US-10-753-195-1	Sequence 1, Appli
8	1790	100.0	1193	9	US-10-752-421-1	Sequence 1, Appli
9	1790	100.0	1193	9	US-10-861-662-2	Sequence 2, Appli
10	1790	100.0	1195	3	US-09-759-143-878	Sequence 878, App
11	1790	100.0	1195	3	US-09-780-669-878	Sequence 878, App
12	1790	100.0	1195	3	US-09-822-827-878	Sequence 878, App
13	1790	100.0	1195	3	US-09-895-793-878	Sequence 878, App
14	1790	100.0	1195	3	US-09-895-814-878	Sequence 878, App
15	1790	100.0	1195	5	US-10-012-896-878	Sequence 878, App
16	1790	100.0	1195	5	US-10-011-095-1	Sequence 1, Appli
17	1790	100.0	1195	5	US-10-010-667A-1	Sequence 1, Appli
18	1790	100.0	1195	5	US-10-205-823-396	Sequence 396, App
19	1790	100.0	1195	6	US-10-144-678A-878	Sequence 878, App
20	1790	100.0	1195	6	US-10-294-025-878	Sequence 878, App
21	1790	100.0	1195	6	US-10-393-590-35	Sequence 35, Appl
22	1790	100.0	1195	6	US-10-393-567-35	Sequence 35, Appl
23	1790	100.0	1195	6	US-10-394-087-35	Sequence 35, Appl
24	1790	100.0	1195	6	US-10-295-027-713	Sequence 713, App
25	1790	100.0	1195	6	US-10-295-027-1130	Sequence 1130, Ap
26	1790	100.0	1195	8	US-10-643-795A-16	Sequence 16, Appl
27	1790	100.0	1195	8	US-10-643-795A-42	Sequence 42, Appl
28	1790	100.0	1195	9	US-10-750-262-1	Sequence 1, Appli
29	1790	100.0	1195	9	US-10-948-518-16	Sequence 16, Appl
30	1790	100.0	1195	9	US-10-948-518-42	Sequence 42, Appl
31	1790	100.0	1195	9	US-10-956-157-1811	Sequence 1811, Ap
32	1790	100.0	1195	9	US-10-956-157-7046	Sequence 7046, Ap
33	1790	100.0	1195	9	US-10-858-887-1	Sequence 1, Appli
34	1790	100.0	1195	9	US-10-631-467-428	Sequence 428, App
35	1790	100.0	1195	10	US-11-051-454-396	Sequence 396, App
36	1790	100.0	1201	7	US-10-425-114-16445	Sequence 16445, A
37	1790	100.0	1277	3	US-09-814-353-19910	Sequence 19910, A
38	1790	100.0	1330	7	US-10-755-889-191	Sequence 191, App
39	1732.5	96.8	1365	8	US-10-830-899-6	Sequence 6, Appli
40	1732.5	96.8	1365	9	US-10-861-662-6	Sequence 6, Appli
41	1724	96.3	1354	8	US-10-723-860-5120	Sequence 5120, Ap
42	1503	84.0	1211	9	US-10-631-467-1300	Sequence 1300, Ap
43	1358.5	75.9	3627	5	US-10-011-095-6	Sequence 6, Appli
44	1358.5	75.9	3627	5	US-10-010-667A-6	Sequence 6, Appli
45	1358.5	75.9	3627	6	US-10-165-044-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-696-639-15
; Sequence 15, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-15

Alignment Scores:

Pred. No.:	1.63e-195	Length:	1177
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-750-262-2 (1-339) x US-10-696-639-15 (1-1177)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 2
US-10-165-044-1
; Sequence 1, Application US/10165044
; Publication No. US20030149531A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappell Mitchell
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158-20016.02
; CURRENT APPLICATION NUMBER: US/10/165,044
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1191)
US-10-165-044-1

Alignment Scores:

Pred. No.:	1.66e-195	Length:	1193
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-750-262-2 (1-339) x US-10-165-044-1 (1-1193)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483
```

```
Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080

RESULT 3
US-10-408-009-1
; Sequence 1, Application US/10408009
; Publication No. US20040072196A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001603
;  CURRENT APPLICATION NUMBER: US/10/408,009
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-408-009-1

Alignment Scores:
Pred. No.:              1.66e-195       Length:         1193
```

```
Score:                  1790.00         Matches:        339
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     7               Gaps:           0

US-10-750-262-2 (1-339) x US-10-408-009-1 (1-1193)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
```

```
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080

RESULT 4
US-10-857-785-1
; Sequence 1, Application US/10857785
; Publication No. US20040219162A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001607
;  CURRENT APPLICATION NUMBER: US/10/857,785
;  CURRENT FILING DATE:  2004-05-28
;  PRIOR APPLICATION NUMBER: US 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: US 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: US 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: US 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-857-785-1

Alignment Scores:
Pred. No.:                1.66e-195       Length:          1193
Score:                    1790.00         Matches:         339
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              100.00%         Indels:          0
DB:                       8               Gaps:            0

US-10-750-262-2 (1-339) x US-10-857-785-1 (1-1193)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080

RESULT 5
US-10-856-109-1
; Sequence 1, Application US/10856109
; Publication No. US20040219591A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001606
;  CURRENT APPLICATION NUMBER: US/10/856,109
;  CURRENT FILING DATE:  2004-05-28
;  PRIOR APPLICATION NUMBER: US 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: US 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: US 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: US 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
```

; LOCATION: (64)...(1083)
US-10-856-109-1

Alignment Scores:

Pred. No.:	1.66e-195	Length:	1193
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-750-262-2 (1-339) x US-10-856-109-1 (1-1193)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

RESULT 6
US-10-830-899-2
; Sequence 2, Application US/10830899
; Publication No. US20040253232A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Etessami, Soudabeh
; APPLICANT: Challita-Eid, Pia M.
; APPLICANT: Perez-Villar, Juan
; APPLICANT: Meyrick Morrison, Karen Jane
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Faris, Mary
; APPLICANT: Gudas, Jean
; APPLICANT: Raitano, Arthur B.
; TITLE OF INVENTION: Antibodies and Molecules Derived
; TITLE OF INVENTION: therefrom that Bind to STEAP-1 Proteins
; FILE REFERENCE: 51158-20016.26
; CURRENT APPLICATION NUMBER: US/10/830,899
; CURRENT FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 10/010,667
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/011,095
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 10/236,878
; PRIOR FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)...(1085)
US-10-830-899-2

Alignment Scores:

Pred. No.:	1.66e-195	Length:	1193
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-10-750-262-2 (1-339) x US-10-830-899-2 (1-1193)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
```

```
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100

Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120

Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140

Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160

Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180

Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200

Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220

Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240

Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260

Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280

Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300

Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320

Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339

Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

```
RESULT 7
US-10-753-195-1
; Sequence 1, Application US/10753195
; Publication No. US20050004349A1
; GENERAL INFORMATION:
;  APPLICANT: Agensys, Inc.
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas Saffran
;  APPLICANT:  Daniel E.H. Afar
;  APPLICANT:  Steven Chappell Mitchell
;  APPLICANT:  Mary Faris
;  APPLICANT:  Aya Jakobovits
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 51158-20016.02
;  CURRENT APPLICATION NUMBER: US/10/753,195
;  CURRENT FILING DATE:  2004-01-06
;  PRIOR APPLICATION NUMBER: US/10/165,044
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: US 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: US 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: WO 99/62941
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: PCT/US00/33040
;  PRIOR FILING DATE: 2000-12-06
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1191)
US-10-753-195-1

Alignment Scores:
Pred. No.:                1.66e-195      Length:          1193
Score:                    1790.00        Matches:         339
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       8              Gaps:            0

US-10-750-262-2 (1-339) x US-10-753-195-1 (1-1193)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20

Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40

Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60

Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80

Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100

Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120

Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140

Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160

Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180

Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
```

```
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

RESULT 8
US-10-752-421-1
; Sequence 1, Application US/10752421
; Publication No. US20050063975A1
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001612
; CURRENT APPLICATION NUMBER: US/10/752,421
; CURRENT FILING DATE: 2004-01-05
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-752-421-1

Alignment Scores:

Pred. No.:	1.66e-195	Length:	1193
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-10-750-262-2 (1-339) x US-10-752-421-1 (1-1193)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy         61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

RESULT 9
US-10-861-662-2
; Sequence 2, Application US/10861662
; Publication No. US20050086707A1

```
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Etessami, Soudabeh
;  APPLICANT:  Challita-Eid, Pia M.
;  APPLICANT:  Perez-Villar, Juan
;  APPLICANT:  Meyrick Morrison, Karen Jane
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Faris, Mary
;  APPLICANT:  Gudas, Jean
;  APPLICANT:  Raitano, Arthur B.
;  TITLE OF INVENTION: Antibodies and Molecules Derived
;  TITLE OF INVENTION:  therefrom that Bind to STEAP-1 Proteins
;  FILE REFERENCE: 51158-20016.26
;  CURRENT APPLICATION NUMBER: US/10/861,662
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: 10/010,667
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 10/011,095
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 10/236,878
;  PRIOR FILING DATE: 2002-09-06
;  PRIOR APPLICATION NUMBER: 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (66)...(1085)
US-10-861-662-2

Alignment Scores:
Pred. No.:              1.66e-195       Length:         1193
Score:                  1790.00         Matches:        339
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     9               Gaps:           0

US-10-750-262-2 (1-339) x US-10-861-662-2 (1-1193)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 10
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 878
```

; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Alignment Scores:

Pred. No.:	1.67e-195	Length:	1195
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-09-759-143-878 (1-1195)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 11
US-09-780-669-878
; Sequence 878, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-780-669-878

Alignment Scores:

Pred. No.:	1.67e-195	Length:	1195
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-09-780-669-878 (1-1195)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305
```

```
Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 12
US-09-822-827-878
; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-827-878

Alignment Scores:

Pred. No.:	1.67e-195	Length:	1195
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-09-822-827-878 (1-1195)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025
```

```
Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 13
US-09-895-793-878
; Sequence 878, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.534C2
;  CURRENT APPLICATION NUMBER: US/09/895,793
;  CURRENT FILING DATE:  2001-06-29
;  NUMBER OF SEQ ID NOS: 982
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-895-793-878

Alignment Scores:
Pred. No.:                1.67e-195      Length:          1195
Score:                    1790.00        Matches:         339
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       3              Gaps:            0

US-10-750-262-2 (1-339) x US-09-895-793-878 (1-1195)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 14
US-09-895-814-878
; Sequence 878, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
```

```
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C26
;  CURRENT APPLICATION NUMBER: US/09/895,814
;  CURRENT FILING DATE:  2001-06-29
;  NUMBER OF SEQ ID NOS: 990
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-895-814-878

Alignment Scores:
Pred. No.:                1.67e-195      Length:          1195
Score:                    1790.00        Matches:         339
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       3              Gaps:            0

US-10-750-262-2 (1-339) x US-09-895-814-878 (1-1195)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 15
US-10-012-896-878
; Sequence 878, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Wantanabe, Yoshihiro
;  APPLICANT:  Meagher, Madeleine Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C27
;  CURRENT APPLICATION NUMBER: US/10/012,896
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 1011
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-896-878

Alignment Scores:
Pred. No.:                1.67e-195      Length:          1195
Score:                    1790.00        Matches:         339
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       5              Gaps:            0

US-10-750-262-2 (1-339) x US-10-012-896-878 (1-1195)
```

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

Search completed: December 6, 2005, 20:50:02
Job time : 959 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2005, 16:29:58 ; Search time 159 Seconds
(without alignments)
663.545 Million cell updates/sec

Title: US-10-750-262-2
Perfect score: 1790
Sequence: 1 MESRKDITNQEELWKMKPRR.....IRHGWEDVTKINKTEICSQL 339

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10750262/runat_06122005_162948_15696/app_query.fasta_1.519
-DB=Published_Applications_NA_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10750262_@CGN_1_1_121_@runat_06122005_162948_15696
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	107	6.0	3137	6	US-10-793-626-3842	Sequence 3842, Ap
	2	99.5	5.6	2622	6	US-10-750-185-48126	Sequence 48126, A
	3	99.5	5.6	2803	6	US-10-750-185-29256	Sequence 29256, A
	4	93.5	5.2	819	6	US-10-793-626-1307	Sequence 1307, Ap
c	5	92.5	5.2	3263	6	US-10-793-626-3595	Sequence 3595, Ap
	6	90.5	5.1	1179	6	US-10-793-626-3305	Sequence 3305, Ap
	7	90.5	5.1	1564	7	US-11-110-977-1	Sequence 1, Appli
	8	89.5	5.0	1515	6	US-10-467-657-2439	Sequence 2439, Ap
	9	87.5	4.9	340000	7	US-11-102-978-3	Sequence 3, Appli
c	10	87	4.9	3083	6	US-10-793-626-4225	Sequence 4225, Ap
c	11	87	4.9	3301	6	US-10-793-626-4209	Sequence 4209, Ap
c	12	87	4.9	4071	6	US-10-793-626-3381	Sequence 3381, Ap
	13	86	4.8	1068	6	US-10-467-657-4965	Sequence 4965, Ap
	14	85.5	4.8	1138	6	US-10-750-185-36689	Sequence 36689, A
c	15	85.5	4.8	1462	6	US-10-750-185-37763	Sequence 37763, A
c	16	85	4.7	660	6	US-10-793-626-2205	Sequence 2205, Ap
	17	85	4.7	1368	7	US-11-074-176-237	Sequence 237, App
	18	85	4.7	1517	6	US-10-750-185-26344	Sequence 26344, A
c	19	85	4.7	2557	6	US-10-793-626-3829	Sequence 3829, Ap
c	20	85	4.7	3146	6	US-10-793-626-4281	Sequence 4281, Ap
	21	85	4.7	3646	6	US-10-793-626-4070	Sequence 4070, Ap
	22	84	4.7	963	6	US-10-750-185-27964	Sequence 27964, A
	23	83.5	4.7	1470	6	US-10-793-626-2631	Sequence 2631, Ap
c	24	83.5	4.7	3304	6	US-10-793-626-4182	Sequence 4182, Ap
c	25	83.5	4.7	4142	6	US-10-793-626-3523	Sequence 3523, Ap
	26	83	4.6	819	6	US-10-467-657-7791	Sequence 7791, Ap
	27	83	4.6	1636	7	US-11-102-240-77	Sequence 77, Appl
	28	83	4.6	1915	7	US-11-068-686-3	Sequence 3, Appli
	29	83	4.6	1917	7	US-11-074-176-221	Sequence 221, App
c	30	82	4.6	3109	6	US-10-793-626-3708	Sequence 3708, Ap
	31	82	4.6	3149	6	US-10-793-626-3902	Sequence 3902, Ap
	32	81.5	4.6	2007	9	US-11-082-389-401	Sequence 401, App
	33	81.5	4.6	2721	6	US-10-485-517-51	Sequence 51, Appl
	34	81.5	4.6	3514	6	US-10-750-185-44589	Sequence 44589, A
	35	81	4.5	1020	6	US-10-793-626-1693	Sequence 1693, Ap
	36	81	4.5	2419	6	US-10-750-185-49215	Sequence 49215, A
	37	81	4.5	3075	7	US-11-055-822-507	Sequence 507, App
	38	81	4.5	3075	7	US-11-055-822-593	Sequence 593, App
c	39	81	4.5	3806	6	US-10-793-626-4166	Sequence 4166, Ap
c	40	81	4.5	4105	6	US-10-750-185-45307	Sequence 45307, A
	41	80.5	4.5	1406	6	US-10-750-185-38622	Sequence 38622, A
	42	80	4.5	360	7	US-11-174-150-17	Sequence 17, Appl
	43	80	4.5	1347	6	US-10-467-657-677	Sequence 677, App
c	44	80	4.5	3976	6	US-10-750-185-60435	Sequence 60435, A
	45	80	4.5	5099	6	US-10-821-234-193	Sequence 193, App

ALIGNMENTS

RESULT 1
US-10-793-626-3842
; Sequence 3842, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3842
; LENGTH: 3137
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3842

Alignment Scores:

Pred. No.:	0.179	Length:	3137
Score:	107.00	Matches:	64
Percent Similarity:	44.07%	Conservative:	55
Best Local Similarity:	23.70%	Mismatches:	94
Query Match:	5.98%	Indels:	58
DB:	6	Gaps:	17

US-10-750-262-2 (1-339) x US-10-793-626-3842 (1-3137)

```
Qy          64 ThrGlnGluLeuPheProGlnTrp------HisLeuProIleLysIleAlaAlaIleIle 81
Db         105 ACACAACAGGCACCACCACAATGGTTGTATCATTTTTCATTAAGTTTAAGTTTTGTGATT 164

Qy          82 AlaSer---------LeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeu 98
Db         165 GCTCAAGGTCTAATATTAGTTATCTTTTATAAAATGCATCAATCTGTAATAAATGATGTG 224

Qy          99 AlaThrSerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeu 118
Db         225 ------ATGAAGCAACAATGG--------------ATAGTTGCAAAGAATAAAATAATT 263

Qy         119 ProMetValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIle 138
Db         264 AAAATTGTAATAGTTGCGATT------GTCGTATATTTATTATTACTTATAATGCGGGTG 317

Qy         139 ValGlnLeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMet 158
Db         318 ATT-----------GGAACA---------TCATTACCTAATCATTTA---AGTTATCAT 353

Qy         159 LeuThr---------ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHis 175
Db         354 CTCACGCAATACGAACAACGTACGCTAGGGCTATTTAAATCACCATATGTGTTGTTAGTT 413

Qy         176 AlaIleTyrSerLeuSerTyr------ProMetArgArgSerTyrArgTyrLysLeuLeu 193
Db         414 ACTTTTATATCCATGGTATTCTTACGTCCAATGGTAGAACAAATCATTTATAGATATCTC 473

Qy         194 AsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAsp--- 212
Db         474 ------------------------------------------ATCATCCATGAATTA 488

Qy         213 ------ValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeu 230
Db         489 GGAAAAGTATGGAATAGACAATTTGTAATTGGTTTGTCTATTCTTATTGAAACGATCGTA 548

Qy         231 AlaLeuLeuAlaValThrSerIleProSerValSerAspSerLeu---------ThrTrp 247
Db         549 CATGTTTACGACATGTCATCGATTTTTGAAATTTTTCCATATATCGTTATTGCTACGGCA 608

Qy         248 ArgGluPheHisTyrIleGlnSerLysLeuGly---IleValSerLeuLeuLeuGlyThr 266
Db         609 GCTACAATACTATATATTAAATCGCGGGATAATTTAATTGTCGCTTATATATTTCAAGTG 668

Qy         267 IleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIleLysGlnPheVal------ 284
Db         669 ATTTTGCAGTGTATCCTTTT-TATAGAAATTTTATGTAAGTATACCAACTTTTAAGAAGA 727

Qy         285 -----------TrpTyrThrProProThrPheMet---IleAlaValPheLeuProIle 299
Db         728 AAAGTTTGAAAGTGGATAACACCCATACTATTTATAGATATTGTTATTTTTACACCAATC 787

Qy         300 Val---ValLeuIlePheLysSerIleLeu 308
Db         788 ATTGAAGAACTTTTATTTCGTCATTTAATC 817
```

RESULT 2
US-10-750-185-48126
; Sequence 48126, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48126
; LENGTH: 2622
; TYPE: DNA
; ORGANISM: Bovine 19866880404440
US-10-750-185-48126

Alignment Scores:

Pred. No.:	1.02	Length:	2622
Score:	99.50	Matches:	65
Percent Similarity:	36.57%	Conservative:	48
Best Local Similarity:	21.04%	Mismatches:	95
Query Match:	5.56%	Indels:	101
DB:	6	Gaps:	13

US-10-750-262-2 (1-339) x US-10-750-185-48126 (1-2622)

```
Qy          37 MetLeuLysArgProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAsp 56
Db        1472 CTCCTTAATAGACTTCTGTTACTCCACTACCATCACTCCCAAAATGCTGATGAGTTT--- 1528

Qy          57 CysProSerGluLeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLys 76
Db        1529 TGTCTCAAGGAAGAACAGCAT---------------------------------------- 1549

Qy          77 IleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGlu------Val 94
Db        1550 CTTGCATGCAGAGTGTTTGACTCAACTGTTTTTCTTCTGCTTCTTCGTCATCTCTGAGTC 1609

Qy          95 IleHisProLeu-AlaThrSerHisGlnGlnTyrPheTyrLysIle---ProIleLeuVa 113
Db        1610 CTTCGTCCTGTCAGCGATGGCATATGACCGCTATGTGGCCATCTGTAAGCCACTGGTATA 1669

Qy         113 lIleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLeuValTyrLeuProGl 133
Db        1670 CACAGTCACCATGTCTCCTAAGGTCTGTTTACTGCTTTTGTTGGGTGTGTATGTGATGGG 1729

Qy         133 yValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTyrLysLysPheProHisTr 153
Db        1730 GTTTTCAGGGGCCATGGCC------CACACAGGAAGC---------------------- 1760

Qy         153 pLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePhePheAlaVa 173
Db        1761 -----------------------------------ATAGCAAGTCTGATCTTCTGTGC 1783

Qy         173 lLeuHisAlaIleTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLe 193
Db        1784 T-------------------------------------------GACAACCTCAT 1795

Qy         193 uAsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspVa 213
Db        1796 CAATCATTTCTTGTGTGATATCCCTCCTCTGCTTGAGCTGGCTTGCAACAGCTCTTCTGT 1855

Qy         213 lTrpArgMetGluIleTyrValSerLeu---GlyIleValGlyLeuAlaIleLeuAlaLe 232
Db        1856 GCACGAACTGGTGGTCTTCATAGTTGTGACCACTGTTATTGGAATGGTCATTGTCACCAT 1915

Qy         232 uLeuAlaValThrSerIleProSerValSerAspSerLeuThrTrp------------- 247
Db        1916 C--------------------TCCATCTCTTACACTCTAATCCTTTCCAGCATTTCTCC 1954

Qy         248 ------------------------ArgGluPheHisTyrIleGln-SerLysLeuGlyI 259
Db        1955 GCATTCACTCCACTGAGGGCAGATCCAAAGCTTTCAGTACATGCAGCTCCCACATAATTG 2014

Qy         259 leValSerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleA 279
Db        2015 TGGTTTTCCTTTTTTTTGGTTCT---------------------------------- 2037

Qy         279 spIleLysGlnPheValTrpTyrThrProProThrPheMet------------------ 292
```

```
Db       2038 -----GCAGCTTTTGTGTATCTCAAACCACCTTCCGTTTTGCACCTTGACCAAGGGAAAG 2092

Qy        293 --IleAlaValPheLeuProIleValValLeuIlePheLysSerIleLeuPheLeuProC 312

Db       2093 TGTCATCCCTGTTTTATACCATTGTGGTGCCCATGTTAAATCCACTGATATAT------A 2146

Qy        312 ysLeuArgLysLysIleLeuLys 319

Db       2147 GTTTGAGGAACAAGGATGTCAAA 2169
```

RESULT 3
US-10-750-185-29256
; Sequence 29256, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 29256
; LENGTH: 2803
; TYPE: DNA
; ORGANISM: Bovine 19866880686697
US-10-750-185-29256

Alignment Scores:

Pred. No.:	1.13	Length:	2803
Score:	99.50	Matches:	75
Percent Similarity:	34.15%	Conservative:	51
Best Local Similarity:	20.33%	Mismatches:	100
Query Match:	5.56%	Indels:	143
DB:	6	Gaps:	18

US-10-750-262-2 (1-339) x US-10-750-185-29256 (1-2803)

```
Qy          17 LysProArgArgAsnLeuGluGluAsp-----------------AspTyrLeuHisLys 30

Db        1251 AGGAAACAGAGAAGCCTAGAGGAGGATCTAATCAGCTCATGGAATGATTCCCTTAGA--- 1307

Qy          31 AspThrGlyGluThrSerMetLeuLysArgProValLeuLeuHisLeuHisGlnThrAla 50

Db        1308 ------GGGAGGTATTCAGAGCTG---------------------------------- 1325

Qy          51 HisAlaAspGluPheAspCysProSerGluLeu-------------------------- 61

Db        1326 -----------------TGTTCCAGCTCCTTGTGACAGGGAAGAGGCTCTTCTCCAAAA 1367

Qy          62 GlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIleIle 81

Db        1368 GACCACACACAA------------ACTTGGACTTTAGAA---------------------- 1394

Qy          82 AlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThrSer 101

Db        1395 ---------ACAATTGTGGAAAAAAATATGAGGCAACTACCACAC---------AGCAAA 1436

Qy         102 HisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMetVal 121

Db        1437 CATCAGTCACAGTTTTAT---------------------------------CTTTTA 1460

Qy         122 SerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeu 141

Db        1461 TTTGCAACTTTGTGGCAGAAAGCCTTCCTGCAGGAACTCATGGCTGACAGAATATATTAA 1520

Qy         142 HisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThrArg 161

Db        1521 TGTTCTGTTCGCAAG--------------GAATGTGTGGATCGCTTACTGATGTCAAGA 1565

Qy         162 LysGln-----------------------------------------PheGlyLeuLeu 167

Db        1566 AAAGAAATGGAACGGGGCAAAAGAAAGGAATGTCAGGGATTATTTATCATTAACCTTTCC 1625

Qy         168 SerPhePhePheAlaValLeuHis-------------------------AlaIleTyr 178

Db        1626 CTCTTCTTTGTCCCTGTACTCCATCGGTTATTAATCTCTGACAATGTCGTCGCTCTAGCG 1685

Qy         179 SerLeuSerTyrProMetArgArgSerTyrArgTyrLys--------------------- 191

Db        1686 TCTCGTCAACACATAATTAGGAAAGTACTACGGACCAAAGTATACCAGGCCATCATAAGA 1745

Qy         192 ------LeuLeuAsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIle 209

Db        1746 GAGAGGATAAGAAATTGTTTCTACCTTCTGGTTTCTCAGAGACAAGCGACAGATAAAACA 1805

Qy         210 GluHisAspValTrpArg---------------------------------MetGluIle 218

Db        1806 CAACGAGCTTGCTGGCGCCCACAAGCAACCAGTGCCGTGGTAAAGGTAGTGATGGAGAGT 1865

Qy         219 TyrValSerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIle 238

Db        1866 TACTTTCAGTCTCGGCTGACAGAGGTTTCCCTGGTGGCT---CAGCGGGTAAAGAATCTG 1922

Qy         239 ProSerValSerAsp------------SerLeuThrTrpArgGluPheHisTyrIleGln 254

Db        1923 CCTTCAGTGCAGGAGACCAGGGCTCAGTCCCTGGGCTGGGAAGAC------CCTCTGGAG 1976

Qy         255 SerLysLeuGlyIleValSerLeuLeuLeu---------------------------- 264

Db        1977 AAAGGAATGGGAACCTACTCCAGTATTCTTGAGTGGAGAGTTGCGTGGGCAGTAACGGCC 2036

Qy         265 ------GlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIleLysGln 282

Db        2037 TGGAGGGCTACAGTCCACGGGGTCCCAAAGAGTTGGATGAAAGAGTCGGACACTACTGAG 2096

Qy         283 PheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleValValLeu 302

Db        2097 --------------------------------CGACTAACACTTTCACTTCTGGTCTTG 2123

Qy         303 IlePheLysSerIleLeuPheLeuPro 311

Db        2124 GTTGACAGAAGTCTTTTCTGACTTCCC 2150
```

RESULT 4
US-10-793-626-1307
; Sequence 1307, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1307
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-1307

```
Alignment Scores:
Pred. No.:                0.878          Length:          819
Score:                    93.50          Matches:         62
Percent Similarity:       39.47%         Conservative:    43
Best Local Similarity:    23.31%         Mismatches:      82
Query Match:              5.22%          Indels:          79
DB:                       6              Gaps:            16

US-10-750-262-2 (1-339) x US-10-793-626-1307 (1-819)

Qy         64 ThrGlnGluLeuPheProGlnTrp------HisLeuProIleLysIleAlaAlaIleIle 81
Db        202 ACACAACAGGCACCACCACAATGGTTGTATCATTTTTCATTAAGTTTAAGTTTTGTGATT 261

Qy         82 AlaSer---------LeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeu 98
Db        262 GCTCAAGGTCTAATATTAGTTATCTTTTATAAAATGCATCAATCTGTAATAAATGATGTG 321

Qy         99 AlaThrSerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeu 118
Db        322 ------ATGAAGCAACAATGG--------------ATAGTTGCAAAGAATAAAATAATT 360

Qy        119 ProMetValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIle 138
Db        361 AAAATTGTAATAGTTGCGATT------GTCGTATATTTATTATTACTTATAATGCGGGTG 414

Qy        139 ValGlnLeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMet 158
Db        415 ATT-----------GGAACA---------TCATTACCTAATCATTTA---AGTTATCAT 450

Qy        159 LeuThr---------ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHis 175
Db        451 CTCACGCAATACGAACAACGTACGCTAGGGCTATTTAAATCACCATATGTGTTGTTAGTT 510

Qy        176 AlaIleTyrSerLeuSerTyr------ProMetArgArgSerTyrArgTyrLysLeuLeu 193
Db        511 ACTTTTATATCCATGGTATTCTTACGTCCAATGGTAGAACAAATCATTTATAGATATCTC 570

Qy        194 AsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAsp--- 212
Db        571 ----------------------------------------------ATCATCCATGAATTA 585

Qy        213 ------ValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeu 230
Db        586 GGAAAAGTATGGAATAGACAATTT--------------GTAATTGGTTTGTCTATTCTT 630

Qy        231 AlaLeuLeuAlaValThrSerIleProSerValSerAsp---SerLeuThrTrpArgGlu 249
Db        631 -----------ATTGAAACGATCGTACATGTTTACGACATGTCATCGATTTTTGAAATT 678

Qy        250 PheHisTyrIleGlnSerLysLeuGlyIleValSerLeuLeuLeuGlyThrIleHisAla 269
Db        679 TTTCCATATATCGTTATTGCTACGGCAGCTACAATACTATATATTAAATCGCGGGATAAT 738

Qy        270 LeuIlePheAlaTrpAsnLysTrpIleAspIleLysGlnPheValTrpTyrThrProPro 289
Db        739 TTAATTGTCGCTTAT---------------------------------------------- 753

Qy        290 ThrPheMetIleAlaValPheLeuProIleValValLeuIlePheLysSerIleLeuPhe 309
Db        754 --------------------------ATATTTCAAGTGATTTTGCAGTGTATCCTTTTT 786

Qy        310 LeuProCysLeuArgLys 315
Db        787 ATAGAAATTTTATGTAAG 804

RESULT 5
US-10-793-626-3595/c
; Sequence 3595, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3595
;   LENGTH: 3263
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3595

Alignment Scores:
Pred. No.:                9.4            Length:          3263
Score:                    92.50          Matches:         60
Percent Similarity:       38.59%         Conservative:    55
Best Local Similarity:    20.13%         Mismatches:      91
Query Match:              5.17%          Indels:          92
DB:                       6              Gaps:            15

US-10-750-262-2 (1-339) x US-10-793-626-3595 (1-3263)

Qy         98 LeuAlaThrSerHisGlnGlnTyrPheTyrLys----------------------Ile 109
Db       1572 TTGGCTCAATCAAAGAATGAATTTTACCTTAGAAGATTACATTCGTTATTAGGGGTTATT 1513

Qy        110 ProIle--------------------LeuValIleAsn---------------------- 115
Db       1512 CCGATAGGTGCATTTTTAATTGTACACTTAATGGTAAACCATCAAGCAACGCAAGGTGCT 1453

Qy        116 ----------------------------LysValLeuProMetValSerIleThrLeu 125
Db       1452 GAAGCTTTTAATAGAGCTTCAGGATTTATGGAATCTTTACCATTCCTTATTGTGATGGAA 1393

Qy        126 LeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeuHis--------- 142
Db       1392 TTTATACTTATTTATATACCATTGTTATACCATGGTTTGTTCGGTTTACACATCGCATTC 1333

Qy        143 -----------AsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMet 158
Db       1332 ACTGCTAAGGAGAACATCGGGCATTACTCATTATTTAGAAACTGGATG---------TTT 1282

Qy        159 LeuThrArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyr 178
Db       1281 TTCTTCCAACGTGTAAGTGGTATTTTAGCATTTGTTTTTATTGCAATGCACTTA------ 1228

Qy        179 SerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyr--- 197
Db       1227 --------------------------TGGCAAACACGTTTGCAAAAAGCTTTTTATGGT 1195

Qy        198 GlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGlu 217
Db       1194 AAATCTGTGGACTATAATCTAATGCATGAAACATTACAACATCCGTTATGGGCAATC--- 1138

Qy        218 IleTyrValSerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSer 237
Db       1137 TTTTACATT-----------------ATTTGTGTCATTGCTGTTGTTTTCCATTTTGCT 1096

Qy        238 IleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeu 257
Db       1095 AATGGTTTATGGTCATTTTGTGTAACATGG---------GGCTTTTTACAATCTAAAAAA 1045

Qy        258 Gly--------------------------IleValSerLeuLeuLeuGlyThrIleHis 268
Db       1044 TCACAACGTGTTTTTACTTGGATTTCACTCATAGTATTTTTAGTGATTTCTTATATTGGT 985

Qy        269 ---AlaLeuIlePheAlaTrp--------------------------AsnLysTrpIle 278
Db        984 GTTGCAGCCGTTATTGCGTTTATATAAGTATACGAATTTTCATTTTGAAACAAGCGAGTA 925
```

```
Qy        279 AspIle----------LysGlnPheValTrpTyrThrProProThrPheMetIleAla 294
Db        924 TAGATAAATTTACTACTTAGAAATTATGAAACGTTAAAAATTAACTGTTTCGTATTTAGT 865

Qy        295 ValPheLeuProIleValVal----------LeuIlePheLysSerIleLeuPheLeu 310
Db        864 TTATATCTGAAATTAAAAGTAGGGCTTTAGATTTAAATATTCAGGGGAGTGACATTTCTA 805

Qy        311 ProCysLeuArgLysLysIleLeuLysIle-ArgHisGlyTrpGluAspVal 327
Db        804 TGGCAGAGAAAAAAATTATTGTTGTCGGTGGAGGACTAGCTGGTCTGATGTC 753

RESULT 6
US-10-793-626-3305
; Sequence 3305, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3305
;   LENGTH: 1179
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3305

Alignment Scores:
Pred. No.:                3.43          Length:          1179
Score:                    90.50         Matches:         56
Percent Similarity:       40.56%        Conservative:    45
Best Local Similarity:    22.49%        Mismatches:      75
Query Match:              5.06%         Indels:          73
DB:                       6             Gaps:            15

US-10-750-262-2 (1-339) x US-10-793-626-3305 (1-1179)

Qy         39 LysArgProValLeuLeuHisLeuHisGlnThrAlaHisAlaAsp------GluPheAsp 56
Db        541 AAAGAAGATGAATTGTCACATCCAAATCAAACACCTCGTTCATCTAGTATTGAATCACAA 600

Qy         57 CysProSerGluLeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLys 76
Db        601 ACTGGCTCAAGCGTCATAAGACCTCGTGAGGTTTTTAAA------TATCTGATGATTACA 654

Qy         77 IleAlaAlaIleIleAla---SerLeuThrPheLeuTyrThrLeuLeuArgGluValIle 95
Db        655 TTTTTAGTGCTGGTTGCTAATTCTGTAACATTCGTGTTT----------------ATT 696

Qy         96 HisProLeuAlaThrSer------HisGlnGlnTyrPheTyrLysIleProIleLeuVal 113
Db        697 AATCCATTAATTTTATCCAATGGACATGAAATGTCTTTTGTGTCTTTAGCACTACTTGTT 756

Qy        114 IleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLeuValTyrLeuProGly 133
Db        757 ---AATGGTGTAGCAGGTGTGATTGGTACTTCA----------------TTAGGCGGT 795

Qy        134 ValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTyrLysLysPheProHisTrp 153
Db        796 GTTTTATCT---------------------------------------------------- 804

Qy        154 LeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSerPhe---PhePheAla 172
Db        805 ---GATAAGTTT------ACTAGTAAGCGTTGGTTAATAATTTCGATTTCAATATTTATA 855

Qy        173 ValLeuHisAlaIleTyrSerLeuSerTyrPro----------------MetArgArgSer 187
Db        856 ATAATGATGATAATTCTTAACTTATTATTACCAGGAACAGGATTATTATTAGTTGGCTTA 915

Qy        188 TyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAla 207
Db        916 TTTATGTGGAATTTAATGCAGTGGAGTACAAATCCAGCTATTCAAAGTGGTATTATTGAA 975

Qy        208 TrpIleGluHisAspVal----------------TrpArgMetGluIleTyrValSerLeu 222
Db        976 CACGTCGAAGGAGATACAAGCCAAGTGATGAGTTGGAATATGTCG---------AGTCTC 1026

Qy        223 ----------------------GlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaVal 235
Db       1027 AATGCCGGTATTGGCGTTGGCGGAATCGTAGGTGGACTCGTTATGACACATTTATCAGTG 1086

Qy        236 ThrSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSer 255
Db       1087 GAATATGTTACT----------------------------------TATACTAGTGCA 1110

Qy        256 LysLeuGlyIleValSerLeuLeuLeu 264
Db       1111 TTGATAGGTTTAATTAGTCTTATCATT 1137

RESULT 7
US-11-110-977-1
; Sequence 1, Application US/11110977
; Publication No. US20050260682A1
; GENERAL INFORMATION:
;  APPLICANT: Charmley, Patrick R.
;  APPLICANT:  Smith, Ryan C.
;  APPLICANT:  Argonza-Barrett, Rhodora H.
;  APPLICANT:  Fitzgibbon, Matthew P.
;  APPLICANT:  Wang, Kai P.
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing or Treating Psoriasis
;  FILE REFERENCE: CECH118764
;  CURRENT APPLICATION NUMBER: US/11/110,977
;  CURRENT FILING DATE:  2005-04-19
;  PRIOR APPLICATION NUMBER: US/10/112,645
;  PRIOR FILING DATE: 2002-03-28
;  PRIOR APPLICATION NUMBER: US 60/280,514
;  PRIOR FILING DATE: 2001-03-29
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (314)..(1138)
;   OTHER INFORMATION:
US-11-110-977-1

Alignment Scores:
Pred. No.:                5.26          Length:          1564
Score:                    90.50         Matches:         42
Percent Similarity:       39.91%        Conservative:    49
Best Local Similarity:    18.42%        Mismatches:      75
Query Match:              5.06%         Indels:          62
DB:                       7             Gaps:            8

US-10-750-262-2 (1-339) x US-11-110-977-1 (1-1564)

Qy        134 ValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTyrLysLysProHisTrp 153
Db        286 GTGTTGAGTAAACAGACCAAGTTGGATCATGGGGAATTTCAGAGGTCATGCCCTCCCTGG 345

Qy        154 LeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePhePheAlaVal 173
Db        346 --------------------------------AACCTTCTTTTTTATTATTGGTCTTTG 372
```

```
Qy        174 LeuHisAlaIleTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLeu 193
              :::                                                 ||||||
Db        373 GTG-------------------------------------------GTGTACAAAGAGTAT 390

Qy        194 AsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspVal 213
              :::      |||   |||       :::             :::|||   ::::::   :::
Db        391 TCTGAAGTATATCTGCAAAAAGCAAAAGCGAACCTGCTATCTTGGTTCCAAAACATTATT 450

Qy        214 -TrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLe 233
               :::|||:::||||||        :::  |||||||||:::|||:::      :::
Db        451 CTATCGATTGGAAATTTTGGAGGGAATTACAATAGTTGGCATGGCTTTAACTGGCATGGC 510

Qy        233 uAlaValThrSerIleProSer------------------------------------- 240
                        ||||||
Db        511 TGGGGAGCAGTTTATTCCTGGAGGGCCCCATCTGATGTTATATGACTATAAACAAGGTCA 570

Qy        241 -ValSerAspSerLeuThrTrpArgGluPhe------HisTyrIleGlnSerLysLeuGl 258
               :::      |||   |||       |||      ::::::              |||||
Db        571 CTGGAATCAACTCCTGGGCTGGCATCATTTCACCATGTATTTCTTCTTTGGGCTGTTGGG 630

Qy        258 yIleValSerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrp-- 277
              |:::      :::|||      ||||||   :::|||      :::      |||
Db        631 TGTGGCAGATATCTTATGTTTCACCATCAGTTCACTTCCTGTGTCCTTAACCAAGTTAAT 690

Qy        278 ------------IleAspIleLysGlnPheValTrpTyr------ThrProProThrPh 291
                          :::   ::::::   |||::::::|||      |||
Db        691 GTTGTCAAATGCCTTATTTGTGGAGGCCTTTATCTTCTACAACCACACTCATGGCCGGGA 750

Qy        291 eMetIleAlaValPheLeuPro------IleValValLeuIlePhe-------------- 304
               |||:::   :::|||:::        :::|||::::::::|||
Db        751 AATGCTGGACATCTTTGTGCACCAGCTGCTGGTTTTGGTCGTCTTTCTGACAGGCCTCGT 810

Qy        305 ----------------------LysSerIleLeuPheLeuProCysLeuArgLysLysIl 317
                                   ::::::   :::   |||      ||||||      ::
Db        811 TGCCTTCCTAGAGTTCCTTGTTCGGAACAATGTACTTCTGGAGCTATTGCGGTCAAGTCT 870

Qy        317 eLeuLysIleArgHisGlyTrp 324
              ::::   ::::::      |||
Db        871 CATTCTGCTTCAGGGGAGCTGG 892
```

RESULT 8
US-10-467-657-2439
; Sequence 2439, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2439
; LENGTH: 1515
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2439

Alignment Scores:			
Pred. No.:	6.56	Length:	1515
Score:	89.50	Matches:	85
Percent Similarity:	36.86%	Conservative:	51
Best Local Similarity:	23.04%	Mismatches:	133
Query Match:	5.00%	Indels:	100
DB:	6	Gaps:	19

US-10-750-262-2 (1-339) x US-10-467-657-2439 (1-1515)

```
Qy         19 ArgArgAsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeu 38
              |||:::||||||      |||
Db        252 CGGCAAAACCTTTTTTCAGACGGC---------------------------------- 275

Qy         39 LysArgProValLeuLeuHis------LeuHisGlnThrAlaHisAlaAspGluPheAsp 56
                    |||      :::|||      :::   |||       |||   |||:::   |||
Db        276 AATCACCCTGCCTTTGTGCATCCCCGCATTTGTCAGCTGTTTCACCTGGATCAGCCTGAC 335

Qy         57 CysProSerGluLeu-----------------GlnHisThrGlnGluLeu-PheProGl 70
              |||                            :::                 ||| ||||||
Db        336 CTTCCGCGTCGAAGGATTTTGGGGGACAGTGATGATTATGAGCCTGTCCTCGTTTCCGCT 395

Qy         70 nTrpHisLeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLe 90
                 :::||||||::::::   |||              ||||||::::::
Db        396 CGCCTACCTGCCCGTCGAGGCGGCACTCAAACGCATCAGCCTGTCTTAC----------- 444

Qy         90 uLeuArgGluValIleHisProLeuAlaThrSerHisGlnGlnTyrPheTyrLysIlePr 110
                    ||||||          |||       |||       |||   |||:::
Db        445 ----GAAGAAGTCAGCCTGTCCTTGGGCAAAAGCCGCCTGCAAACCTTTTTTTCC----- 495

Qy        110 oIleLeuValIleAsnLysValLeuProMetVal------SerIleThrLeuLeuAlaLe 128
                    ::::::   ::::::   |||   :::       |||:::   |||:::||||||
Db        496 ----GCCATCCTCCCACAGCTCAAACCCGCCATCGGCAGCAGCGTGTTACTGATCGCCCT 551

Qy        128 uValTyrLeu---------------------------------ProGlyValIleAlaAl 137
              |      |||                                 |||           ||
Db        552 GCATATGCTGGTCGAATTTGGCGCGGTATCCATTTTGAACTACCCCACTTTTACCACTGC 611

Qy        137 aIleValGlnLeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTr 157
              ||||   |||   :::             |||                     |||
Db        612 CATTTTCCAAGAATACGAA---ATGTCCTACAACAACAATACCGCCGCCCTGCTTTCCGC 668

Qy        157 pMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAla-- 176
               :::||||||          |||::::::   |||       ::::::
Db        669 TGTTTTGACG---GCGGTGTGCGGCATCGTCGTATTTGGAGAAAGCATATTTCGCGGCAA 725

Qy        177 -------IleTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAs 194
                    ||||||               :::   |||   |||       |||   |||
Db        726 AGCCAAGATTTACCACAGCGGCAAAGGCGTTGCCCGTCCTTATCCCGTCAAAACCCTC-- 783

Qy        194 nTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTr 214
                                          |||               |||       |||::
Db        784 --------------------------AAACTGCCCGGTCAGATCGGCGCGATTGTTTT 815

Qy        214 pArgMetGluIleTyrValSerLeuGlyIleVal---------GlyLeuAlaIleLeuAl 231
               :         :::   :::   ||||||||||:::         |||:::   |||
Db        816 TTTAAGCAGCTTGTTGATT---TTGGGCATTATTATCCCCTTTGGCGTATTGATACATTG 872

Qy        231 aLeuLeuAlaValThrSer------------IleProSerValSerAspSerLeuThrTr 247
               ::::::      ||||||            :::   ||||||   |||:::
Db        873 GATGATGGTCGGCACTTCCGGCACATTCGCGCTCGTATCCGTATTTGATGCC-------- 924

Qy        247 pArgGluPheHisTyrIleGlnSer---LysLeuGlyIleValSerLeuLeuLeuGlyTh 266
                          :::|||:::|||      :::       :::       :::|||
Db        925 ------------TTTATCCGTTCCTTAAGCGTATCGGCTTTAGGTGCGATTTTGACTAT 971

Qy        266 rIleHisAlaLeuIlePheAlaTrp--------------------------AsnLysTr 277
               :::   ||||||      |||                            ||
Db        972 ATTATGTGCCTTGCCCCTTGTTTGGGCATCGGTTCGCTATCGCAATTTTTTAACCGTTTG 1031

Qy        277 pIleAspIleLysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLe 297
               |||||||          |||:::   :::       |||       :::||||||:::   ||
Db       1032 GATAGACAGGCTGCCGTTTTTACTGCACGCCGTCCCCGGTTTGGTTATCGCCCTATCCTT 1091

Qy        297 uPro---------------------------------------IleValValLeuIl 303
              |                                          |||||||||:::::
Db       1092 GGTTTATTTCAGCATCAACTACACCCCTGCCGTTTACCAAACCTTTATCGTCGTCATCCT 1151

Qy        303 ePheLysSerIleLeuPheLeuPro------------CysLeuArgLysLysIleLeuLy 319
               :         :::|||:::||||||          ||||||      :::   ::
Db       1152 TGCCTATTTCATGCTTTACCTGCCGATGGCGCAAACCACCCTGAGGACTTCCTTGGAACA 1211
```

```
Qy        319 sIleArgHisGlyTrpGluAspVal 327
              ::::      |||   |||   |||
Db       1212 ACTCCCCAAAGGGATGGAACAGGTC 1236
```

RESULT 9
US-11-102-978-3
; Sequence 3, Application US/11102978
; Publication No. US20050250142A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Technology Transfer Office
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
; FILE REFERENCE: 0274-5537.1US
; CURRENT APPLICATION NUMBER: US/11/102,978
; CURRENT FILING DATE: 2005-04-11
; PRIOR APPLICATION NUMBER: PCT/US2003/033152
; PRIOR FILING DATE: 2003-10-18
; PRIOR APPLICATION NUMBER: 60/419,576
; PRIOR FILING DATE: 2002-10-18
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 340000
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (56948)..(57115)
;   OTHER INFORMATION: C21orf34 exon
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (80006)..(81089)
;   OTHER INFORMATION: Gene VDAC2P; voltage-dependent anion channel isoform 2 pseudogene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (167308)..(167438)
;   OTHER INFORMATION: C21orf34 exon
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (216732)..(216833)
;   OTHER INFORMATION: C21orf34 exon
US-11-102-978-3

Alignment Scores:

Pred. No.:	4.23e+04	Length:	340000
Score:	87.50	Matches:	69
Percent Similarity:	37.54%	Conservative:	44
Best Local Similarity:	22.92%	Mismatches:	87
Query Match:	4.89%	Indels:	102
DB:	7	Gaps:	17

US-10-750-262-2 (1-339) x US-11-102-978-3 (1-340000)

```
Qy         57 CysPro-SerGluLeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLy 76
              ||||||  |||   :::              :::|||      |||          :::
Db     183992 TGTCCACTCCAGAATTTATTTTTTTGACAATGTTTTTCTTTTCTGGAAATTTTAATTGAT 184051

Qy         76 sIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHi 96
              :::   |||      :::::::::   ||||||   |||||||||      |||:::
Db     184052 TCTCATCGCC---ACTTCAAATGTTTTATTTCTACTTACTTTGTTACACATTGTATTG-- 184106

Qy         96 sProLeuAlaThrSerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLy 116
                                                :::      ||||||   :::||
Db     184107 ----------------------------------ATGTTATTTCTTGTCTCTTCCAA 184129

Qy        116 sValLeuProMetVal------SerIleThrLeuLeuAlaLeuValTyrLeuProGlyVa 134
              |:::|||      :::      |||   :::      ||||||::::::
Db     184130 AATCCTAGCATGCTTATTTTGAAGTTATTCTGAAACCGCTCTATTATTT----------- 184178

Qy        134 lIleAlaAlaIleValGln---LeuHisAsnGlyThrLysTyrLys-------------- 148
                 :::   :::::::::   ||||||              |||
Db     184179 ----TCATGTCTTCTGGAATAACTTCACTGAATGTTGTTTTTAAAATTTTGCTGGTGCCT 184234

```
Qy   149 -------LysPheProHisTrpLeuAspLysTrpMet------LeuThr------ArgLy 162
                      ||| ||| |||::: ||| |||||| |||::
Db   184235 TTTTATATCATTCTCTCATGGCTTAGAATTTTGGTTTTCAGGCTTAACTGGAATGAGAAG 184294

Qy   162 s------GlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLe 180
              :   :::||| ||| |||:::|||||| ||| ||
Db   184295 GATTTAAAAATTCTCTCTCTCTCTCTCATTGCTAGCCCTTCTGCACCATTCCTATTGTCT 184354

Qy   180 uSer--------------------TyrProMetArgArgSerTyrArgTyrLysLeuLe 193
              |||| :::|||::: ||| |||
Db   184355 TAGTGTTGGCTCTGTACCCTCTCGTTTCCCAGTC--------------TATAATCTCTG 184399

Qy   193 uAsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspVa 213
                 ||| ||||||::: ||| :::   ::: |||||
Db   184400 CTAATGGGGATATCAAAAACCTAGTC--ACTAAATCAAAGAGCAGTCTGTCCCAGGATGT 184457

Qy   213 l------------Trp--------------------ArgMetGluIleTyrValSerLe 222
              | ||| ||| :::::::||| |||
Db   184458 GACTGTGAGATTATGGCTGCTTGCTTTGGCCTCCCCAAGAAAGCAGCTCTATGCAAGCCG 184517

Qy   222 uGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSerValSe 242
               ||| :::||| ||| ||
Db   184518 TGGCTCCAGGAAAAGGGAGGTGTTAGTCAGTTGT-----------------TCGGCTTC 184559

Qy   242 rAspSerLeuThrTrpArg-- 248
              | ||||||:::|||
Db   184560 CTCTTGTCTTACCTTCAGGTTTTAATCAGTAAGCTTGGCACTGATTATTACTCCCTGTGG 184619

Qy   249 ------------GluPheHisTyrIleGlnSerLysLeuGlyIleValSerLeuLeuLe 264
                          ::::::   ::::::::::|||::::: |||:::||
Db   184620 GACACATGTGGCATCCAGTTACTTTGCAGATACAAGGATTGGCTTGCTT---CTCATTCT 184676

Qy   264 uGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIleLysGlnPheVa 284
              | ||||||
Db   184677 AGACACCATC-- 184686

Qy   284 lTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleValValLeuIlePh 304
              ||| ::: ||| |||::: |||::: ||| |||:::||
Db   184687 -TGGTGCAGTGTACCTCACTTTGTGTTTATAGTTTATTTCTGGTATGTTTATCTTGTTTT 184745

Qy   304 e 304
              |
Db   184746 T 184746

RESULT 10
US-10-793-626-4225/c
; Sequence 4225, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4225
;   LENGTH: 3083
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4225

Alignment Scores:

Pred. No.:	37.9	Length:	3083
Score:	87.00	Matches:	80
Percent Similarity:	32.58%	Conservative:	35
Best Local Similarity:	22.66%	Mismatches:	103
Query Match:	4.86%	Indels:	135

```
DB:                    6              Gaps:          20

US-10-750-262-2 (1-339) x US-10-793-626-4225 (1-3083)

Qy         58 ProSerGluLeuGlnHisThrGlnGluLeuProGlnTrp--------------His 72
              ||||||   :::   |||                   |||              :::
Db       2931 CCAAGTTCAATGTTGCATGAGCAT------------GGATGGAGCGGTATCAATTTCAAT 2884

Qy         73 LeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu--- 91
              |||           ||||||:::      |||   :::|||      ||||||
Db       2883 TCACCATTTGCAGATATGGCAATTTTATTAGGTCTTAACTGGTTAGCAATATTACTTTAT 2824

Qy         92 ---ArgGluValIleHisProLeuAlaThr------------------------------ 100
                 |||:::   |||       |||
Db       2823 ATGGAAGCAGTTGTGTCACCGTTTGGTACTGGAGTTTCTTTTGTTGCCGTTACTGGACGT 2764

Qy        101 ------------------------SerHisGlnGlnTyrPhe------------------ 106
                                       |||           |||
Db       2763 GTGTTACGCGCTATGGAAGAAAATGGGCATATTCCTAAATTCTTAGGTAAAATTAATAAA 2704

Qy        107 ---TyrLysIleProIleLeuValIle------AsnLysValLeuProMetValSerIle 123
                 |||   ||||||   :::   |||       |||   ::::::   |||:::   :::
Db       2703 AAGTATAATATCCCACGTGTTGCCATTGCATTTAATGCAATTATCAGCATGATTATGGTG 2644

Qy        124 ThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeuHisAsn 143
              ||||||                        |||   :::||||||::::::
Db       2643 ACATTGTTCCGTGACTGG---------GGTACACTAGCTGCGGTTATTTCTACTGCAACA 2593

Qy        144 GlyThrLysTyr--------------------------------LysLysPheProHis 152
                 |||                                     |||     |||
Db       2592 TTAGTTGCATATTTAACTGGTCCAACTACGGTTATTTCATTACGTAAAATGGCACCA--- 2536

Qy        153 TrpLeuAspLysTrpMetLeuThrArg--------------------LysGlnPheGly 165
                          :::||||||                        |||
Db       2535 --------------AAAATGACTCGTCCATTTAAAGCTAATATTTTAAAATTTATGGCA 2491

Qy        166 LeuLeuSerPhePhePheAlaValLeuHisAlaIleTyr--------------------- 178
                 |||||||||       |||   |||   |||||||||
Db       2490 CCTTTATCCTTTGTTTTAGCATCATTA---GCTATCTATTGGGCAATGTGGCCAACAACA 2434

Qy        179 --------------------SerLeuSerTyrProMetArgArgSerTyrArgTyrLys 191
                                   |||       |||:::           |||   ||||||
Db       2433 GCAGAAGTTATTTTAATTATTATTTTAGGTTTACCTATTTATTTCTTCTATGAATATAAA 2374

Qy        192 LeuLeuAsnTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHis 211
                 ::::||||||          :::   :::|||                  ||||||
Db       2373 ---ATGAATTGGAAGAATACTAAA---AAACAAATTGGCGGAAGCTTATGGATT------ 2326

Qy        212 AspValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeuAla 231
                                                 |||:::   |||   :::||||||
Db       2325 ---------------------------------ATTATCTATCTTATTGTTCTCGCA 2302

Qy        232 LeuLeuAlaValThrSerIleProSerValSerAspSerLeuThrTrpArgGluPheHis 251
                 |||:::                                |||   |||        |||
Db       2301 TTCTTATCATTTATTGGAAGTAAAGAGTTCAAA---GGCTTAAATTGG------ATTCAC 2251

Qy        252 TyrIleGlnSerLysLeuGlyIleVal-SerLeuLeuLeuGlyThrIleHisAlaLeuIl 271
              |||           |||   |||||| |||||||||      :::|||:::   :::
Db       2250 TATCCATGGGATTTCTTAGTCATTGTAATCGTTGCTTTAATCTTCTATCAACTAGGTA-- 2193

Qy        271 ePheAlaTrpAsnLysTrpIleAspIleLysGlnPheVal------------------- 284
                       :::   :::   :::|||   |||:::
Db       2192 ------------CGACAAGTTACTTTGAAAGTATTTATTTCAAGCGTGCGAACAAGTTG 2146

Qy        285 ----------TrpTyrThrProProThrPheMetIleAlaValPheLeuProIleValVa 301
                        |||
Db       2145 AATAAGAAAATGG---------------------------------------------- 2133

Qy        301 lLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIleAr 321
                       :::|||      :::         :::|||:::::::::|||||
Db       2132 ------------GCGATAAGTTGCGTAAAACACGCAAAAAAGCGCGTCATAAAGATTGG 2086

Qy        321 gHisGlyTrpGluAspValThrLysIleAsnLysThr 333
```

```
                                  |||   :::|||||||||||||||
Db       2085 AAAGAACGCGATCGACAAGAGCAAAATCAATAAGACG 2049

RESULT 11
US-10-793-626-4209/c
; Sequence 4209, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4209
;   LENGTH: 3301
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4209

Alignment Scores:
Pred. No.:                42.1          Length:              3301
Score:                    87.00         Matches:             67
Percent Similarity:       35.71%        Conservative:        38
Best Local Similarity:    22.79%        Mismatches:          95
Query Match:              4.86%         Indels:              94
DB:                       6             Gaps:                13

US-10-750-262-2 (1-339) x US-10-793-626-4209 (1-3301)

Qy         73 LeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu-Ar 92
              ||||||:::|||   |||   |||:::   |||   ||||||           |||   ||
Db       2526 CTTCCGGTAAAGTGGGCAAAAATATTGCTAAGTGAGACCTTTGCTATTAAATTAGCATAG 2467

Qy         92 gGluValIleHisProLeuAlaThrSerHisGlnGlnTyrPheTyr------------Ly 108
              |   :::                                   |||   |||        ::
Db       2466 GTCTCTT-----------------------------TATTTGTATTTAAACTAAAAGGA 2437

Qy        108 sIleProIleLeuValIleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLe 128
              ::::      :::       :::   :::||||||  :::   :::   ||||||   ||
Db       2436 GTTGTCCACAATGGATCCGAGTTTGATTTTACCTTATTTATGGGTA---CTTTTAGTACT 2380

Qy        128 uValTyrLeuProGlyValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTyrLy 148
              ||||:::|||   |||::::::||||||        :::                   ||
Db       2379 TGTATTTTTAGAAGGATTATTAGCAGCTGATAATGCAATTGTAATGGCGGTAATGGTTAA 2320

Qy        148 sLysPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSe 168
              |   |||                |||       |||              :::||||||||||
Db       2319 ACATCTACCACCTAAACAACGTAAAAAAGCACTTTTT---------TATGGCCTATTAGG 2269

Qy        168 rPhePhePheAlaValLeuHisAlaIleTyrSerLeuSer---------------------- 181
                 |||                |||::::::   :::|||
Db       2268 TGCATTCATTTTTAGATTTATTGCTTTATTTTTAATAAGTATTATTGCAAACTTCTGGTG 2209

Qy        182 ----------------------TyrProMetArgArgSerTyrArgTyrLysLeuLeuAs 194
                                   |||   ::      |||   :::      |||
Db       2208 GATTCAAGCAGCAGGTGCTGTTTACTTAATCTATATGTCTATTAAA---AATTTATGGCA 2152

Qy        194 nTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHis-------- 211
                 :::   :::|||     :::::::::   ::::::         ||||||
Db       2151 ATTTTTCCATCAGTCAAATGAAAAACACCATAAAGAAACAGGAGACGAACATCATTTCGA 2092

Qy        212 --------------------------------AspValTrpArgMetGluIleTyrVa 220
                                              |||                   ||
Db       2091 TGAAACAGGCAACGAAAAAGAAGTAGGCCCTAAATCTTTTTGGGGAACAGTATTTAAAGT 2032

Qy        220 lSerLeuGlyIleValGlyLeuAlaIle---------LeuAlaLeuLeuAlaVal---Th 236
```

```
Db       2031 TGAATTCGCTGATATCGCGTTTGCAATTGATTCGATGCTTGCCGCATTAGCCATAGCCGT 1972

Qy        236 rSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLy 256
Db       1971 TACATTACCAAAAGTTGGC--------------------ATACATTTTGGTGGTATGGA 1933

Qy        256 sLeuGly------IleValSerLeuLeuLeuGlyThrIleHisAlaLeuIle-------- 271
Db       1932 CTTAGGCCAATTTATTGTTATGTTCCTTGGTGGAATGATAGGTGTCATCTTGATGAGATT 1873

Qy        272 ----------------------------------------------------------Ph 272
Db       1872 TGCAGCAACTTGGTTTGTAGAATTGTTGAATAAATATCCAGGACTTGAAGGTGCTGCGTT 1813

Qy        272 eAlaTrpAsnLysTrpIleAspIleLysGlnPheVal-TrpTyrThrProProThrPheM 292
Db       1812 TGCAATTGTAGGTTGGGTAGGTATTAAACTTGTTATAATGGTAC---------------- 1769

Qy        292 etIleAlaValPheLeuProIleValValLeuIlePhe 304
Db       1768 --------------TTGCACATCCTGATATTGGCGTTT 1745

RESULT 12
US-10-793-626-3381/c
; Sequence 3381, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
;  APPLICANT: KIMMERLY, WILLIAM JOHN
;  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;  FILE REFERENCE: PU3480US
;  CURRENT APPLICATION NUMBER: US/10/793,626
;  CURRENT FILING DATE:  2004-03-04
;  PRIOR APPLICATION NUMBER: 60/164,258
;  PRIOR FILING DATE: 1999-11-09
;  NUMBER OF SEQ ID NOS: 4472
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3381
;  LENGTH: 4071
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: synthetic
;  OTHER INFORMATION: nucleic acid sequence
US-10-793-626-3381

Alignment Scores:
Pred. No.:              57.9          Length:          4071
Score:                  87.00         Matches:         67
Percent Similarity:     35.71%        Conservative:    38
Best Local Similarity:  22.79%        Mismatches:      95
Query Match:            4.86%         Indels:          94
DB:                     6             Gaps:            13

US-10-750-262-2 (1-339) x US-10-793-626-3381 (1-4071)

Qy          73 LeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeu-Ar 92
Db        1305 CTTCCGGTAAAGTGGGCAAAAATATTGCTAAGTGAGACCTTTGCTATTAAATTAGCATAG 1246

Qy          92 gGluValIleHisProLeuAlaThrSerHisGlnGlnTyrPheTyr------------Ly 108
Db        1245 GTCTCTT----------------------------TATTTGTATTTAAACTAAAAGGA 1216

Qy         108 sIleProIleLeuValIleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLe 128
Db        1215 GTTGTCCACAATGGATCCGAGTTTGATTTTACCTTATTTATGGGTA---CTTTTAGTACT 1159

Qy         128 uValTyrLeuProGlyValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTyrLy 148
Db        1158 TGTATTTTTAGAAGGATTATTAGCAGCTGATAATGCAATTGTAATGGCGGTAATGGTTAA 1099

Qy         148 sLysPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSe 168
Db        1098 ACATCTACCACCTAAACAACGTAAAAAAGCACTTTTT---------TATGGCCTATTAGG 1048

Qy         168 rPhePhePheAlaValLeuHisAlaIleTyrSerLeuSer---------------------- 181
Db        1047 TGCATTCATTTTTAGATTTATTGCTTTATTTTTAATAAGTATTATTGCAAACTTCTGGTG 988

Qy         182 ----------------------TyrProMetArgArgSerTyrArgTyrLysLeuLeuAs 194
Db         987 GATTCAAGCAGCAGGTGCTGTTTACTTAATCTATATGTCTATTAAA---AATTTATGGCA 931

Qy         194 nTrpAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHis-------- 211
Db         930 ATTTTTCCATCAGTCAAATGAAAAACACCATAAAGAAACAGGAGACGAACATCATTTCGA 871

Qy         212 ---------------------------------AspValTrpArgMetGluIleTyrVa 220
Db         870 TGAAACAGGCAACGAAAAAGAAGTAGGCCCTAAATCTTTTTGGGGAACAGTATTTAAAGT 811

Qy         220 lSerLeuGlyIleValGlyLeuAlaIle---------LeuAlaLeuLeuAlaVal---Th 236
Db         810 TGAATTCGCTGATATCGCGTTTGCAATTGATTCGATGCTTGCCGCATTAGCCATAGCCGT 751

Qy         236 rSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLy 256
Db         750 TACATTACCAAAAGTTGGC--------------------ATACATTTTGGTGGTATGGA 712

Qy         256 sLeuGly------IleValSerLeuLeuLeuGlyThrIleHisAlaLeuIle-------- 271
Db         711 CTTAGGCCAATTTATTGTTATGTTCCTTGGTGGAATGATAGGTGTCATCTTGATGAGATT 652

Qy         272 ----------------------------------------------------------Ph 272
Db         651 TGCAGCAACTTGGTTTGTAGAATTGTTGAATAAATATCCAGGACTTGAAGGTGCTGCGTT 592

Qy         272 eAlaTrpAsnLysTrpIleAspIleLysGlnPheVal-TrpTyrThrProProThrPheM 292
Db         591 TGCAATTGTAGGTTGGGTAGGTATTAAACTTGTTATAATGGTAC---------------- 548

Qy         292 etIleAlaValPheLeuProIleValValLeuIlePhe 304
Db         547 --------------TTGCACATCCTGATATTGGCGTTT 524

RESULT 13
US-10-467-657-4965
; Sequence 4965, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
;  APPLICANT: CHIRON SpA
;  APPLICANT: FONTANA Maria Rita
;  APPLICANT: PIZZA Mariagrazia
;  APPLICANT: MASIGNANI Vega
;  APPLICANT: MONACI Elisabetta
;  TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
;  FILE REFERENCE:
;  CURRENT APPLICATION NUMBER: US/10/467,657
;  CURRENT FILING DATE:  2003-08-11
;  PRIOR APPLICATION NUMBER: GB-0103424.8
;  PRIOR FILING DATE: 2001-02-12
;  NUMBER OF SEQ ID NOS: 9218
;  SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4965
;  LENGTH: 1068
;  TYPE: DNA
;  ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4965

Alignment Scores:
Pred. No.:              9.9           Length:          1068
Score:                  86.00         Matches:         67
Percent Similarity:     37.09%        Conservative:    45
Best Local Similarity:  22.19%        Mismatches:      112
Query Match:            4.80%         Indels:          78
```

```
DB:                    6              Gaps:          15

US-10-750-262-2 (1-339) x US-10-467-657-4965 (1-1068)

Qy          77 IleAlaAlaIleIleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHis 96
Db         193 ATGTCTGTGATGGTGTTTTCCTTGATTTTGTTGTTGGCATTATTGTTGATTATTGTCCCT 252

Qy          97 ProLeuAlaThrSerHisGlnGlnTyrPheTyrLysIleProIleLeuVal--------- 113
Db         253 ATGCTGGTCGGGCAGTTCAATAATTTGGCATCTCGCCTGCCCCAATTAATCGGTTTTATG 312

Qy         114 IleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLeuValTyrLeu---Pro 132
Db         313 CAGAACACGCTGCTGCCGTGGTTGAAAAATACAATCGGCGGATATGTGGAAATCGATCAG 372

Qy         133 GlyValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTyrLysLysPheProHis 152
Db         373 GCATCTATTATTGCGTGGTTTCAGGCGCATACGGGCGAGTTGAGCAACGCGCTTAAGGCG 432

Qy         153 TrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSerPhePhePheAla 172
Db         433 TGGTTTCCCGTTTTGATG---------AAACAGGGCGGC-----------------AAT 465

Qy         173 ValLeuHisAlaIleTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeu 192
Db         466 ATTGTCAGCAGTATCGGCAACCTGCTGCTGCCGCCCTTGCTGCTTTAC---TATTTCCTG 522

Qy         193 LeuAsnTrp------------------------------------------------------ 195
Db         523 CTGGATTGGCAGCGGTGGTCGTGCGGCATCGCCAAACTGGTTCCGAGGCGTTTTGCCGGT 582

Qy         196 AlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArg 215
Db         583 GCTTATACGCGCATTACGGGTAATTTGAACGAGGTATTGGGCGAATTTTTGCGCGGTCAG 642

Qy         216 MetGluIleTyrValSerLeuGlyIleVal---------GlyLeuAlaIleLeuAlaLeu 232
Db         643 CTTCTGGTGATGCTGATTATGGGCTTGGTTTACGGTTTGGGATTGATGCTAGTCGGACTG 702

Qy         233 LeuAlaValThrSerIleProSerValSerAspSerLeuThrTrpArgGluPheHisTyr 252
Db         703 GATTCGGGATTTGCCATCGGTATGGTTGCCGGTATTTTGGTGTTTGTCCCCTAT------ 756

Qy         253 IleGlnSerLysLeuGly---IleValSerLeuLeuLeuGlyThrIleHisAlaLeuIle 271
Db         757 ------------TTGGGTGCGTTTACGGGATTGCTGCTTGCCACTGTTGCAGCCTTGCTC 804

Qy         272 ------PheAlaTrpAsnLysTrpIleAspIleLysGlnPheValTrpTyrThrProPro 289
Db         805 CAGTTCGGTTCGTGGAACGGAATCTTG------------GCTGTTTGG---------GCG 843

Qy         290 ThrPheMetIleAlaValPheLeu-----------------ProIleValVal------ 301
Db         844 GTTTTTGCCGTCGGTCAGTTTCTCGAAAGTTTTTTCATTACGCCGAAAATTGTAGGAGAC 903

Qy         302 ----------------------LeuIlePheLysSerIleLeuPhe------------ 309
Db         904 CGTATCGGCCTGTCGCCGTTTTGGGTTATCTTTTCGCTGATGGCGTTCGGAGAGCTGATG 963

Qy         310 ----------------------LeuProCysLeuArgLysLysIleLeuLysIleArg 321
Db         964 GGCTTTGTCGGAATGTTGGCCGGATTGCCTTTGGCCGCCGTAACCTTGGTCTTGCTTCGC 1023

Qy         322 HisGly 323
Db        1024 GAGGGC 1029

RESULT 14
US-10-750-185-36689
; Sequence 36689, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 36689
;   LENGTH: 1138
;   TYPE: DNA
;   ORGANISM: Bovine  19866880906331
US-10-750-185-36689

Alignment Scores:
Pred. No.:                12.5          Length:          1138
Score:                    85.50         Matches:         68
Percent Similarity:       36.34%        Conservative:    53
Best Local Similarity:    20.42%        Mismatches:      122
Query Match:              4.78%         Indels:          91
DB:                       6             Gaps:            12

US-10-750-262-2 (1-339) x US-10-750-185-36689 (1-1138)

Qy          38 LeuLysArgProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCys 57
Db          79 CTCCGGAGAGTACTTCAGGTTTTAACCCACTTGACATGGTAATGGGATCAAGCTTACTGT 138

Qy          58 ProSerGluLeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLys--- 76
Db         139 CTTAATTGAATGTACTTTCACTTTGCAATAATTAGCCCTTCACATATTCCAGTAAACTTA 198

Qy          77 --------------------------------IleAlaAlaIleIleAlaSerLeuThr 85
Db         199 AAAAGCTTCAGTAAAGATATCTCAAATACTCATATAAGTAGAGTGTTCTTTTCATTGGAT 258

Qy          86 PheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThrSerHisGlnGlnTyr 105
Db         259 TTCATCAAGACTCTTGTG-----------------------------TTTATAGATGCA 288

Qy         106 PheTyrLysIleProIleLeuValIle------------AsnLysValLeuProMetVal 121
Db         289 TTTGGCAAAGCATAGATTTTATTTTTGGACTTGTTTTCCAATGCTCTTTCTCCTAATATT 348

Qy         122 SerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeu 141
Db         349 TACTGTGTGATCTTGAGTAAG--------------------GCAGCACTGTTCTAATTA 387

Qy         142 HisAsnGlyThrLys--------------------TyrLysLysPhe------------ 150
Db         388 CAAGATGGTAATAATCTTATCTATAATGAGTTTCTCTATAGGAGATTCACTGGCATAGAG 447

Qy         151 ------------ProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeu 166
Db         448 TTGACACTCAATCCATCGTGGCTT---------------------------------- 471

Qy         167 LeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeuSerTyrProMetArgArg 186
Db         472 ------TTTTGGTTTTGTTTTGTTCTTTCTATATTCTCCTGAGTTCTAACATATCACGCT 525

Qy         187 SerTyrArgTyrLysLeu-Leu---AsnTrp---------------------------- 195
Db         526 TCAGTAAGATATAAAATATATGCATAGCTGGTAGAAAGACACTTTCAAGATACAGTTTCA 585

Qy         196 ----------AlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAs 212
```

```
Db        586 TTGATACATATCATTTCCACATGTACAAGAAAATAGTTTTAACCAAGCAGTTGCAAAGGG 645

Qy        212 pValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeuAlaLe 232

Db        646 CATGTGGGTGGTGCTTATCAGTGGCGGTTCATCTAGTGGGAATATGGTTTTTATAGCATG 705

Qy        232 uLeuAlaValThrSerIleProSerValSerAspSerLeuThrTrp---------- 247

Db        706 TCTAGTAGTGATTGCTGTAGCCCACCAACATAATCTGCTTCACTGGTGTTTACCTGAGAC 765

Qy        248 -ArgGluPheHisTyrIleGlnSerLysLeuGlyIleValSerLeuLeuLeuGlyThrIl 267

Db        766 AGCAGAATTTTTTATGTCTCTCAGTATCCTGAATATTGCAAAAGAAATCTTCCATATTTT 825

Qy        267 eHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIleLysGlnPheValTrpTyrTh 287

Db        826 GCATTT-TTGTTTTACTACCATGATTCAGAAATTCCATGTTTAGGGTTTCATTGGAAAGA 884

Qy        287 rProProThrPheMetIleAlaValPheLeuProIleValValLeuIlePheLysSer-- 306

Db        885 G--------------CTCAGTGTATTTCACCTGGTTAAGGTTCTTGAAATCGCCTCAAA 929

Qy        307 -------IleLeuPheLeuProCysLeuArgLysLys 316

Db        930 CTGATGAACCCTATGGATTCCCTGTGTTCAACAGAAA 966

RESULT 15
US-10-750-185-37763/c
; Sequence 37763, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 37763
;   LENGTH: 1462
;   TYPE: DNA
;   ORGANISM: Bovine  19866881070185
US-10-750-185-37763

Alignment Scores:
Pred. No.:              18.3          Length:         1462
Score:                  85.50         Matches:        46
Percent Similarity:     39.00%        Conservative:   32
Best Local Similarity:  23.00%        Mismatches:     78
Query Match:            4.78%         Indels:         44
DB:                     6             Gaps:           7

US-10-750-262-2 (1-339) x US-10-750-185-37763 (1-1462)

Qy        105 TyrPheTyrLysIlePro-IleLeuValIleAsnLysValLeuProMetValSerIleTh 124

Db       1426 TATTGGTACTATGGCCCACCTATATGCCATTGATAAACTAACAAAAGTTGTTAGTAGTTT 1367

Qy        124 rLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGlnLeuHisAsnGl 144

Db       1366 TTGGATATTGTCCAATCACCTAGCTACCTGGTTTGCCACCTGTCTAAGTGTTTTCTACTT 1307

Qy        144 yThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGln-- 163

Db       1306 CTTTAAAGTAGCCAACTTCTCCCACCCCTGCTTCACTTGGCTGCGGTGGCGAATTCGTAG 1247

Qy        164 -------------------PheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIl 177

Db       1246 TGTGGTACTGGTGCTTCTCTTGGGGTCTTTGTCCTTACTGTTTTTGAATTATGAATCAAT 1187

Qy        177 eTyrSerLeuSerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsn------Tr 195

Db       1186 ATATACACTTAGTCATATCTTAACTAACAGCTACAAAATATATGTAAGAAACTCAACGTG 1127

Qy        195 pAlaTyrGlnGlnValGlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpAr 215

Db       1126 GTCC-----------------------TCAGATGTAAGTGAAACTCATTATCTTCACCA 1091

Qy        215 gMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaVa 235

Db       1090 GTTGATTGTTTTTAACTTCATCAACTTAATCCCCTTT-----------CTTCTGTCCCT 1043

Qy        235 lThrSerIle---------------------------------------------------- 238

Db       1042 GACCTCACTGCTCCTCTTAGTTCTCTCCTTGATGAGACACATCAGGAATTTGCAGTTCAA 983

Qy        239 -ProSerValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGl 258

Db        982 CCCCAGCTCAAAGGATCTCAGCACA------GAGGCCCATAAAAGAGCCATGAAAATCGT 929

Qy        258 yIleValSerLeuLeuLeuGlyThrIleHisAla---------LeuIlePheAlaTrp 274

Db        928 GATGTCTTTCCTCTTCCTCTTCATCATTCATGTCTCTTCCATCCTATTAATAGCTTGG 871

Search completed: December  6, 2005, 18:50:55
Job time : 320 secs
```

This Page Blank (uspto)

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 6, 2005, 16:29:53 ; Search time 200 Seconds
(without alignments)
3012.967 Million cell updates/sec

Title: US-10-750-262-2
Perfect score: 1790
Sequence: 1 MESRKDITNQEELWKMKPRR.....IRHGWEDVTKINKTEICSQL 339

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool_h/US10750262/runat_06122005_162946_15642/app_query.fasta_1.519
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10750262_@CGN_1_1_193_@runat_06122005_162946_15642 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1790	100.0	1193	3	US-09-455-486-1	Sequence 1, Appli
2	1790	100.0	1195	3	US-09-323-873A-1	Sequence 1, Appli
3	1790	100.0	1195	3	US-09-685-166A-878	Sequence 878, App
4	1790	100.0	1195	3	US-09-679-426-878	Sequence 878, App
5	1790	100.0	1195	3	US-09-759-143-878	Sequence 878, App
6	1790	100.0	1195	3	US-10-010-667A-1	Sequence 1, Appli
7	1790	100.0	1195	3	US-10-012-896-878	Sequence 878, App
8	1782	99.6	1147	3	US-09-949-016-2686	Sequence 2686, Ap
9	1358.5	75.9	3627	3	US-09-323-873A-6	Sequence 6, Appli
10	1358.5	75.9	3627	3	US-09-455-486-4	Sequence 4, Appli
11	1358.5	75.9	3627	3	US-10-010-667A-6	Sequence 6, Appli
12	1071.5	59.9	9073	3	US-09-949-016-14428	Sequence 14428, A
c 13	905	50.6	592	3	US-09-439-313-342	Sequence 342, App
c 14	905	50.6	592	3	US-09-352-616A-342	Sequence 342, App
c 15	905	50.6	592	3	US-09-636-215-342	Sequence 342, App
c 16	905	50.6	592	3	US-09-685-166A-342	Sequence 342, App
c 17	905	50.6	592	3	US-09-679-426-342	Sequence 342, App
c 18	905	50.6	592	3	US-09-759-143-342	Sequence 342, App
c 19	905	50.6	592	3	US-09-651-236-342	Sequence 342, App
c 20	905	50.6	592	3	US-09-657-279-342	Sequence 342, App
c 21	905	50.6	592	3	US-10-012-896-342	Sequence 342, App
22	741	41.4	2714	3	US-09-562-930-5	Sequence 5, Appli
23	741	41.4	3884	3	US-09-562-930-10	Sequence 10, Appl
24	717	40.1	2453	3	US-09-455-486-5	Sequence 5, Appli
25	717	40.1	2469	3	US-10-104-047-1185	Sequence 1185, Ap
26	715	39.9	1403	3	US-10-012-896-995	Sequence 995, App
27	713.5	39.9	1886	3	US-09-562-930-1	Sequence 1, Appli
28	651	36.4	2118	3	US-09-562-930-3	Sequence 3, Appli
c 29	637.5	35.6	1203	3	US-09-544-618-6	Sequence 6, Appli
30	625	34.9	4429	3	US-09-455-486-7	Sequence 7, Appli
c 31	607	33.9	848	3	US-10-012-896-993	Sequence 993, App
32	576	32.2	519	3	US-10-010-667A-7	Sequence 7, Appli
33	576	32.2	521	3	US-09-323-873A-7	Sequence 7, Appli
34	497	27.8	1213	3	US-09-083-521-3	Sequence 3, Appli
35	450	25.1	455	3	US-09-621-976-9264	Sequence 9264, Ap
c 36	400	22.3	366	3	US-09-030-607-215	Sequence 215, App
c 37	400	22.3	366	3	US-09-439-313-215	Sequence 215, App
c 38	400	22.3	366	3	US-09-352-616A-215	Sequence 215, App
c 39	400	22.3	366	3	US-09-232-149A-215	Sequence 215, App
c 40	400	22.3	366	3	US-09-159-812-215	Sequence 215, App
c 41	400	22.3	366	3	US-09-636-215-215	Sequence 215, App
c 42	400	22.3	366	3	US-09-685-166A-215	Sequence 215, App
c 43	400	22.3	366	3	US-09-115-453-215	Sequence 215, App
c 44	400	22.3	366	3	US-09-688-489-215	Sequence 215, App
c 45	400	22.3	366	3	US-09-679-426-215	Sequence 215, App

ALIGNMENTS

RESULT 1
US-09-455-486-1
; Sequence 1, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-I1
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-09-455-486-1

Alignment Scores:

Pred. No.:	1.09e-202	Length:	1193
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-10-750-262-2 (1-339) x US-09-455-486-1 (1-1193)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

RESULT 2
US-09-323-873A-1
; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-1

Alignment Scores:

Pred. No.:	1.09e-202	Length:	1195
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-09-323-873A-1 (1-1195)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605
```

```
Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 3
US-09-685-166A-878
; Sequence 878, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-685-166A-878

Alignment Scores:
Pred. No.:                1.09e-202      Length:          1195
Score:                    1790.00        Matches:         339
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0

Query Match:              100.00%        Indels:          0
DB:                       3              Gaps:            0

US-10-750-262-2 (1-339) x US-09-685-166A-878 (1-1195)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

```
RESULT 4
US-09-679-426-878
; Sequence 878, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C20
;  CURRENT APPLICATION NUMBER: US/09/679,426
;  CURRENT FILING DATE:  2000-10-02
;  NUMBER OF SEQ ID NOS:  895
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-679-426-878

Alignment Scores:
Pred. No.:                1.09e-202     Length:          1195
Score:                    1790.00       Matches:         339
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              100.00%       Indels:          0
DB:                       3             Gaps:            0

US-10-750-262-2 (1-339) x US-09-679-426-878 (1-1195)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 5
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
```

US-09-759-143-878

Alignment Scores:

Pred. No.:	1.09e-202	Length:	1195
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-09-759-143-878 (1-1195)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 6
US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1

Alignment Scores:

Pred. No.:	1.09e-202	Length:	1195
Score:	1790.00	Matches:	339
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-10-010-667A-1 (1-1195)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 7
US-10-012-896-878
; Sequence 878, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Wantanabe, Yoshihiro
;  APPLICANT:  Meagher, Madeleine Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C27
;  CURRENT APPLICATION NUMBER: US/10/012,896
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 1011
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-896-878

Alignment Scores:
Pred. No.:                1.09e-202      Length:          1195
Score:                    1790.00        Matches:         339
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       3              Gaps:            0

US-10-750-262-2 (1-339) x US-10-012-896-878 (1-1195)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845
```

```
Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 8
US-09-949-016-2686
; Sequence 2686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2686
;   LENGTH: 1147
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2686

Alignment Scores:
Pred. No.:              9.12e-202       Length:         1147
Score:                  1782.00         Matches:        338
Percent Similarity:     99.71%          Conservative:   0
Best Local Similarity:  99.71%          Mismatches:     1
Query Match:            99.55%          Indels:         0
DB:                     3               Gaps:           0

US-10-750-262-2 (1-339) x US-09-949-016-2686 (1-1147)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 92

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 152

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db        153 CCTGTGCTTTTGCATTTGCAGCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 212

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 272

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 332

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 392

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 452

Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 512

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 572

Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 632

Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 692

Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 752

Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIleGlnSerLysLeuGlyIleVal 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 812

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 872

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 932

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 992

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1049

RESULT 9
US-09-323-873A-6
; Sequence 6, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Kahan Leong
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Steve Chappell Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 129.16USU2
;  CURRENT APPLICATION NUMBER: US/09/323,873A
;  CURRENT FILING DATE:  1999-06-01
;  PRIOR APPLICATION NUMBER: 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 3627
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-323-873A-6
```

Alignment Scores:

Pred. No.:	1.17e-150	Length:	3627
Score:	1358.50	Matches:	338
Percent Similarity:	29.68%	Conservative:	0
Best Local Similarity:	29.68%	Mismatches:	1
Query Match:	75.89%	Indels:	801
DB:	3	Gaps:	1

US-10-750-262-2 (1-339) x US-09-323-873A-6 (1-3627)

```
Qy        1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
Db       96 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy       21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
Db      156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy       41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
Db      216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy       61 LeuGlnHisThrGlnGluLeuPheProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
Db      276 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335

Qy       81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
Db      336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 395

Qy      101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
Db      396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 455

Qy      121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
Db      456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 515

Qy      141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
Db      516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 575

Qy      161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
Db      576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635

Qy      181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
Db      636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 695

Qy      201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
Db      696 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 755

Qy      221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
Db      756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 815

Qy      241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIle---------- 253
Db      816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATAT-TCAGGTAAATAATATATAAAA 874

Qy      253 ---------- 253
Db      875 TAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTACCC 934

Qy      253 ---------- 253
Db      935 CATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATTAATAAT 994

Qy      253 ---------- 253
Db      995 GTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAA 1054

Qy      253 ---------- 253
Db     1055 TAAAAGGCATTAAAATATTCTTTGTTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTT 1114

Qy      253 ---------- 253
Db     1115 GTTTGTTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCATGCTGGAGTACAGTGGCACGAT 1174

Qy      253 ---------- 253
Db     1175 CTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTCTCTTGCCTCAGCCTCCTG 1234

Qy      253 ---------- 253
Db     1235 AGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTAGA 1294

Qy      253 ---------- 253
Db     1295 GACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCC 1354

Qy      253 ---------- 253
Db     1355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCT 1414

Qy      253 ---------- 253
Db     1415 TTCTAATATTTGAAACTTGTTAGACAATTTGCTACCCATCTAATGTGATATTTTAGGAAT 1474

Qy      253 ---------- 253
Db     1475 CCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACCTGTCACCTGAATTT 1534

Qy      253 ---------- 253
Db     1535 AGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGA 1594

Qy      253 ---------- 253
Db     1595 AATAATAGAGTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTT 1654

Qy      253 ---------- 253
Db     1655 CCAGCTTACATTTTATATACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA 1714

Qy      253 ---------- 253
Db     1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGTAGATTATCCATAAGAAGAGTGAT 1774

Qy      253 ---------- 253
Db     1775 GTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAATTTAATTCAG 1834

Qy      253 ---------- 253
Db     1835 TCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCA 1894

Qy      253 ---------- 253
Db     1895 GACATTCGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCAT 1954

Qy      253 ---------- 253
Db     1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTA 2014

Qy      253 ---------- 253
Db     2015 CAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAGCCTGATAACCACTGGAGTTCTT 2074

Qy      253 ---------- 253
Db     2075 TGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGATGAACA 2134
```

```
Qy        253 ------------------------------------------------------------ 253
Db       2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTAC 2194
Qy        253 ------------------------------------------------------------ 253
Db       2195 TATATGTACAATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT 2254
Qy        253 ------------------------------------------------------------ 253
Db       2255 CAACCAATGACATGTATTTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA 2314
Qy        253 ------------------------------------------------------------ 253
Db       2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAACTTAGCTATTT 2374
Qy        253 ------------------------------------------------------------ 253
Db       2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCTGG 2434
Qy        253 ------------------------------------------------------------ 253
Db       2435 CAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGT 2494
Qy        253 ------------------------------------------------------------ 253
Db       2495 TGTCAGAACACCGTTGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTG 2554
Qy        253 ------------------------------------------------------------ 253
Db       2555 TAGTGACAAAGCATCCCAATGCAGGCTGAAATGTTTCATCACATCTCTGGATCTCTCTAT 2614
Qy        253 ------------------------------------------------------------ 253
Db       2615 TTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATCAGAATATTTGATTT 2674
Qy        253 ------------------------------------------------------------ 253
Db       2675 TTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAAT 2734
Qy        253 ------------------------------------------------------------ 253
Db       2735 CACATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAA 2794
Qy        253 ------------------------------------------------------------ 253
Db       2795 TCTTCAATCTACCTATATTTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCT 2854
Qy        253 ------------------------------------------------------------ 253
Db       2855 GCAGTGATCCTGCTATAAGTAAGACTCAGTCCCTGATTTTAGGTATCCTGTGAAAAGCAG 2914
Qy        253 ------------------------------------------------------------ 253
Db       2915 AATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAGGGGATGAACA 2974
Qy        253 ------------------------------------------------------------ 253
Db       2975 AAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGA 3034
Qy        253 ------------------------------------------------------------ 253
Db       3035 ATTTTGTTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGAT 3094
Qy        253 ------------------------------------------------------------ 253
Db       3095 AGGCAAAAAGAGCAGAAAGATGTGAATGGACATTGTTGAGAAATGTGATAGGAAAACAAT 3154
Qy        253 ------------------------------------------------------------ 253
Db       3155 CATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAGATGAGGTAGGATGGGATAAACT 3214
```

```
Qy        254 ------------------------------------GlnSerLysLeuGlyIleVal 260
                                                   ||||||||||||||||||||
Db       3215 CTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGAATTGTT 3274

Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3275 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 3334

Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3335 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 3394

Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3395 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 3454

Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3455 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 3511
```

RESULT 10
US-09-455-486-4
; Sequence 4, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-I1
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-486-4

Alignment Scores:

Pred. No.:	1.17e-150	Length:	3627
Score:	1358.50	Matches:	338
Percent Similarity:	29.68%	Conservative:	0
Best Local Similarity:	29.68%	Mismatches:	1
Query Match:	75.89%	Indels:	801
DB:	3	Gaps:	1

US-10-750-262-2 (1-339) x US-09-455-486-4 (1-3627)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 395
Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 455
Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 515
Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 575
Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635
Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 695
Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 755
Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 815
Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIle---------------------- 253
              |||||||||||||||||||||||||||||||||
Db        816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATAT-TCAGGTAAATAATATATAAAA 874
Qy        253 ---------------------------------------------------------- 253
Db        875 TAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTACCC 934
Qy        253 ---------------------------------------------------------- 253
Db        935 CATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATTAATAAT 994
Qy        253 ---------------------------------------------------------- 253
Db        995 GTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAA 1054
Qy        253 ---------------------------------------------------------- 253
Db       1055 TAAAAGGCATTAAAATATTCTTTGTTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTT 1114
Qy        253 ---------------------------------------------------------- 253
Db       1115 GTTTGTTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCATGCTGGAGTACAGTGGCACGAT 1174
Qy        253 ---------------------------------------------------------- 253
Db       1175 CTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTCTCTTGCCTCAGCCTCCTG 1234
Qy        253 ---------------------------------------------------------- 253
Db       1235 AGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTAGA 1294
Qy        253 ---------------------------------------------------------- 253
Db       1295 GACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCC 1354
Qy        253 ---------------------------------------------------------- 253
Db       1355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCT 1414
Qy        253 ---------------------------------------------------------- 253
Db       1415 TTCTAATATTTGAAACTTGTTAGACAATTTGCTACCCATCTAATGTGATATTTTAGGAAT 1474

Qy        253 ---------------------------------------------------------- 253
Db       1475 CCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACCTGTCACCTGAATTT 1534
Qy        253 ---------------------------------------------------------- 253
Db       1535 AGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGA 1594
Qy        253 ---------------------------------------------------------- 253
Db       1595 AATAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTT 1654
Qy        253 ---------------------------------------------------------- 253
Db       1655 CCAGCTTACATTTTATATACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA 1714
Qy        253 ---------------------------------------------------------- 253
Db       1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGTAGATTATCCATAAGAAGAGTGAT 1774
Qy        253 ---------------------------------------------------------- 253
Db       1775 GTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAATTTAATTCAG 1834
Qy        253 ---------------------------------------------------------- 253
Db       1835 TCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCA 1894
Qy        253 ---------------------------------------------------------- 253
Db       1895 GACATTCGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCAT 1954
Qy        253 ---------------------------------------------------------- 253
Db       1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTA 2014
Qy        253 ---------------------------------------------------------- 253
Db       2015 CAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAGCCTGATAACCACTGGAGTTCTT 2074
Qy        253 ---------------------------------------------------------- 253
Db       2075 TGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGATGAACA 2134
Qy        253 ---------------------------------------------------------- 253
Db       2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTAC 2194
Qy        253 ---------------------------------------------------------- 253
Db       2195 TATATGTACAATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT 2254
Qy        253 ---------------------------------------------------------- 253
Db       2255 CAACCAATGACATGTATTTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA 2314
Qy        253 ---------------------------------------------------------- 253
Db       2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAACTTAGCTATTT 2374
Qy        253 ---------------------------------------------------------- 253
Db       2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCTGG 2434
Qy        253 ---------------------------------------------------------- 253
Db       2435 CAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGT 2494
Qy        253 ---------------------------------------------------------- 253
Db       2495 TGTCAGAACACCGTTGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTG 2554
```

```
Qy        253 ------------------------------------------------------------ 253
Db       2555 TAGTGACAAAGCATCCCAATGCAGGCTGAAATGTTTCATCACATCTCTGGATCTCTCTAT 2614
Qy        253 ------------------------------------------------------------ 253
Db       2615 TTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATCAGAATATTTGATTT 2674
Qy        253 ------------------------------------------------------------ 253
Db       2675 TTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAAT 2734
Qy        253 ------------------------------------------------------------ 253
Db       2735 CACATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAA 2794
Qy        253 ------------------------------------------------------------ 253
Db       2795 TCTTCAATCTACCTATATTTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCT 2854
Qy        253 ------------------------------------------------------------ 253
Db       2855 GCAGTGATCCTGCTATAAGTAAGACTCAGTCCCTGATTTTAGGTATCCTGTGAAAAGCAG 2914
Qy        253 ------------------------------------------------------------ 253
Db       2915 AATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAGGGGATGAACA 2974
Qy        253 ------------------------------------------------------------ 253
Db       2975 AAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGA 3034
Qy        253 ------------------------------------------------------------ 253
Db       3035 ATTTTGTTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGAT 3094
Qy        253 ------------------------------------------------------------ 253
Db       3095 AGGCAAAAAGAGCAGAAAGATGTGAATGGACATTGTTGAGAAATGTGATAGGAAAACAAT 3154
Qy        253 ------------------------------------------------------------ 253
Db       3155 CATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAGATGAGGTAGGATGGGATAAACT 3214
Qy        254 ----------------------------------------GlnSerLysLeuGlyIleVal 260
                                                      ||||||||||||||||||||
Db       3215 CTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGAATTGTT 3274
Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3275 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 3334
Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3335 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 3394
Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3395 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 3454
Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3455 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 3511

RESULT 11
US-10-010-667A-6
; Sequence 6, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
;  APPLICANT: Afar, Daniel
;  APPLICANT:  Hubert, Rene S.
;  APPLICANT:  Leong, Kahan
;  APPLICANT:  Raitano, Arthur B.
;  APPLICANT:  Saffran, Douglas C.
;  APPLICANT:  Mitchell, Steve Chappell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001601
;  CURRENT APPLICATION NUMBER: US/10/010,667A
;  CURRENT FILING DATE:  2001-12-06
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 3627
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-010-667A-6

Alignment Scores:
Pred. No.:                1.17e-150      Length:          3627
Score:                    1358.50        Matches:         338
Percent Similarity:       29.68%         Conservative:    0
Best Local Similarity:    29.68%         Mismatches:      1
Query Match:              75.89%         Indels:          801
DB:                       3              Gaps:            1

US-10-750-262-2 (1-339) x US-10-010-667A-6 (1-3627)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155
Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215
Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275
Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335
Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 395
Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 455
Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 515
Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 575
Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAlaValLeuHisAlaIleTyrSerLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635
Qy        181 SerTyrProMetArgArgSerTyrArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 695
Qy        201 GlnGlnAsnLysGluAspAlaTrpIleGluHisAspValTrpArgMetGluIleTyrVal 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        696 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 755
Qy        221 SerLeuGlyIleValGlyLeuAlaIleLeuAlaLeuLeuAlaValThrSerIleProSer 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 815
Qy        241 ValSerAspSerLeuThrTrpArgGluPheHisTyrIle---------------------- 253
              ||||||||||||||||||||||||||||||||||||
Db        816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATAT-TCAGGTAAATAATATATAAAA 874
Qy        253 ------------------------------------------------------------ 253
Db        875 TAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGATATAGAATATGTTGACTTTACCC 934
Qy        253 ------------------------------------------------------------ 253
Db        935 CATAAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCCAATTAATAAT 994
Qy        253 ------------------------------------------------------------ 253
Db        995 GTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTTCCTAGACATAAA 1054
Qy        253 ------------------------------------------------------------ 253
Db       1055 TAAAAGGCATTAAAATATTCTTTGTTTTTTTTTTTTTGTTTGTTTGTTTTTTGTTTGTTT 1114
Qy        253 ------------------------------------------------------------ 253
Db       1115 GTTTGTTTTTTTGAGATGAAGTCTCGCTCTGTTGCCCATGCTGGAGTACAGTGGCACGAT 1174
Qy        253 ------------------------------------------------------------ 253
Db       1175 CTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTCTCTTGCCTCAGCCTCCTG 1234
Qy        253 ------------------------------------------------------------ 253
Db       1235 AGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTTAGTAGA 1294
Qy        253 ------------------------------------------------------------ 253
Db       1295 GACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCC 1354
Qy        253 ------------------------------------------------------------ 253
Db       1355 CACCTCGGCCTCCCAAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCT 1414
Qy        253 ------------------------------------------------------------ 253
Db       1415 TTCTAATATTTGAAACTTGTTAGACAATTTGCTACCCATCTAATGTGATATTTTAGGAAT 1474
Qy        253 ------------------------------------------------------------ 253
Db       1475 CCAATATGCATGGTTTATTATTTCTTAAAAAAAATATTCTTTTACCTGTCACCTGAATTT 1534
Qy        253 ------------------------------------------------------------ 253
Db       1535 AGTAATGCCTTTTATGTTACACAACTTAGCACTTTCCAGAAACAAAAACTCTCTCCTTGA 1594
Qy        253 ------------------------------------------------------------ 253
Db       1595 AATAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTT 1654
Qy        253 ------------------------------------------------------------ 253
Db       1655 CCAGCTTACATTTTATATACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAA 1714
Qy        253 ------------------------------------------------------------ 253
Db       1715 ACTATCTCAGATTTACTGAGGTTTATCTTCTGGTGGTAGATTATCCATAAGAAGAGTGAT 1774
Qy        253 ------------------------------------------------------------ 253
Db       1775 GTGCCAGAATCACTCTGGGATCCTTGTCTGACAAGATTCAAAGGACTAAATTTAATTCAG 1834
```

```
Qy        253 ------------------------------------------------------------ 253
Db       1835 TCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCA 1894
Qy        253 ------------------------------------------------------------ 253
Db       1895 GACATTCGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCAT 1954
Qy        253 ------------------------------------------------------------ 253
Db       1955 CTGATTAGTTTGGAAAGTATGCCTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTA 2014
Qy        253 ------------------------------------------------------------ 253
Db       2015 CAACATTCTCACAGAATTTCCTAATTTTGTAGGTTCAGCCTGATAACCACTGGAGTTCTT 2074
Qy        253 ------------------------------------------------------------ 253
Db       2075 TGGTCCTCATTAAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGATGAACA 2134
Qy        253 ------------------------------------------------------------ 253
Db       2135 CTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTAC 2194
Qy        253 ------------------------------------------------------------ 253
Db       2195 TATATGTACAATACCTAGCCCATAATAGGTATACAATACACATTTGGTAAAACTAATTTT 2254
Qy        253 ------------------------------------------------------------ 253
Db       2255 CAACCAATGACATGTATTTTTCAACTAGTAACCTAGAAATGTTTCACTTAAAATCTGAGA 2314
Qy        253 ------------------------------------------------------------ 253
Db       2315 ACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAAACGCAAACTTAGCTATTT 2374
Qy        253 ------------------------------------------------------------ 253
Db       2375 GATTGTATTCACTGGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTTCTGG 2434
Qy        253 ------------------------------------------------------------ 253
Db       2435 CAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGT 2494
Qy        253 ------------------------------------------------------------ 253
Db       2495 TGTCAGAACACCGTTGAGATTACATAGGTGAACAACTATTTTTAAGCAACTTTATTTGTG 2554
Qy        253 ------------------------------------------------------------ 253
Db       2555 TAGTGACAAAGCATCCCAATGCAGGCTGAAATGTTTCATCACATCTCTGGATCTCTCTAT 2614
Qy        253 ------------------------------------------------------------ 253
Db       2615 TTTGTGCAGACATTGAAAAAATTGTTCATATTATTTCCATGTTATCAGAATATTTGATTT 2674
Qy        253 ------------------------------------------------------------ 253
Db       2675 TTTAAAAACATAGGCCAAGTTCATTCACTTCATTATTCATTTATCAAAATCAGAGTGAAT 2734
Qy        253 ------------------------------------------------------------ 253
Db       2735 CACATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAA 2794
Qy        253 ------------------------------------------------------------ 253
Db       2795 TCTTCAATCTACCTATATTTAATTGAGAATCTAAAATGTACAAATCATTGTGTTGATTCT 2854
Qy        253 ------------------------------------------------------------ 253
Db       2855 GCAGTGATCCTGCTATAAGTAAGACTCAGTCCCTGATTTTAGGTATCCTGTGAAAAGCAG 2914
```

```
Qy        253 ------------------------------------------------------------ 253
Db       2915 AATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAGGGGATGAACA 2974
Qy        253 ------------------------------------------------------------ 253
Db       2975 AAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGA 3034
Qy        253 ------------------------------------------------------------ 253
Db       3035 ATTTTGTTCACTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGAT 3094
Qy        253 ------------------------------------------------------------ 253
Db       3095 AGGCAAAAAGAGCAGAAAGATGTGAATGGACATTGTTGAGAAATGTGATAGGAAAACAAT 3154
Qy        253 ------------------------------------------------------------ 253
Db       3155 CATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAGATGAGGTAGGATGGGATAAACT 3214
Qy        254 ----------------------------------------GlnSerLysLeuGlyIleVal 260
                                                      ||||||||||||||||||||
Db       3215 CTTATTGAACCAATCTTCACCAATTTTGTTTTTCTTTTGCAGAGCAAGCTAGGAATTGTT 3274
Qy        261 SerLeuLeuLeuGlyThrIleHisAlaLeuIlePheAlaTrpAsnLysTrpIleAspIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3275 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 3334
Qy        281 LysGlnPheValTrpTyrThrProProThrPheMetIleAlaValPheLeuProIleVal 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3335 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 3394
Qy        301 ValLeuIlePheLysSerIleLeuPheLeuProCysLeuArgLysLysIleLeuLysIle 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3395 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 3454
Qy        321 ArgHisGlyTrpGluAspValThrLysIleAsnLysThrGluIleCysSerGlnLeu 339
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3455 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 3511
```

RESULT 12
US-09-949-016-14428
; Sequence 14428, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14428
; LENGTH: 9073
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14428

Alignment Scores:

Pred. No.:	6.24e-116	Length:	9073
Score:	1071.50	Matches:	309
Percent Similarity:	23.59%	Conservative:	0
Best Local Similarity:	23.59%	Mismatches:	2
Query Match:	59.86%	Indels:	1000
DB:	3	Gaps:	2

US-10-750-262-2 (1-339) x US-09-949-016-14428 (1-9073)

```
Qy         29 HisLysAspThrGlyGluThrSerMetLeuLysArgProValLeuLeuHisLeuHisGln 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db       3049 CATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGCATTTGCAGCAA 3108
Qy         49 ThrAlaHisAlaAspGluPheAspCysProSerGluLeuGlnHisThrGlnGluLeuPhe 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3109 ACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTT 3168
Qy         69 ProGlnTrpHisLeuProIleLysIleAlaAlaIleIleAlaSerLeuThrPheLeuTyr 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3169 CCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTAC 3228
Qy         89 ThrLeuLeuArgGluValIleHisProLeuAlaThrSerHisGlnGlnTyrPheTyrLys 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3229 ACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTTTTATAAA 3288
Qy        109 IleProIleLeuValIleAsnLysValLeuProMetValSerIleThrLeuLeuAlaLeu 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3289 ATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTTGGCATTG 3348
Qy        129 ValTyrLeuProGlyValIleAlaAlaIleValGlnLeuHisAsnGlyThrLysTyrLys 148
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3349 GTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAAGTATAAG 3408
Qy        149 LysPheProHisTrpLeuAspLysTrpMetLeuThrArgLysGlnPheGlyLeuLeuSer 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3409 AAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGT 3468
Qy        169 PhePhePheAlaValLeuHisAlaIleTyrSerLeuSerTyrProMetArgArgSerTyr 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3469 TTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTAC 3528
Qy        189 ArgTyrLysLeuLeuAsnTrpAlaTyrGlnGlnVal---------------------- 200
              ||||||||||||||||||||||||||||||||||
Db       3529 AGATACAAGTTGCTAAACTGGGCATATCAACAGGT-AAGATGACAGTGTTGACACTGTTA 3587
Qy        200 ------------------------------------------------------------ 200
Db       3588 CTAATAAAAAGTCTAAGTCACCTAACAAATTAATCATTTCTCATTGTAATATCAATACCC 3647
Qy        200 ------------------------------------------------------------ 200
Db       3648 CAACCCTGTTGAAACTCTGTGTTGAAAAAGTCATCTATTTTAAAATTTTTATTATAATTA 3707
Qy        200 ------------------------------------------------------------ 200
Db       3708 CACTAGGGCTTGGTTGTCAGTCGGTTTTATATTGAGAAATGTTTTTTAGGCTGAAAATAA 3767
Qy        200 ------------------------------------------------------------ 200
Db       3768 GGTACAACTTTAGCAACATAAGAAACATTTTGTTCATGGACGAGGCCATATTTCAAACTT 3827
Qy        200 ------------------------------------------------------------ 200
Db       3828 CTACCACCCTCACAAGATTACTTTTTAATATTGTTGTTCTTCTCCTTGTTTACCAATATG 3887
Qy        200 ------------------------------------------------------------ 200
Db       3888 CATGCACATTACAGTTCTATCCAAGTAAACCATCAAATAATTATTAGAAAATTAATAGAT 3947
Qy        200 ------------------------------------------------------------ 200
Db       3948 TATGGAAGTGTTGCATTCAAGAAAAAAAGTGATAGCTCCTATGTCATTTGTCTTAGAGGA 4007
Qy        200 ------------------------------------------------------------ 200
Db       4008 ATGCAAAAAAAAAAAAAAGAAAAAGTCATAAATTTGTGGAGACCTGTTATCAGGGCTTCAT 4067
Qy        200 ------------------------------------------------------------ 200
Db       4068 AGTAGGCACAGGGAAGAGTGTAGAAGGAGATTCACATTCAGGAAATAACTGTTGTTTGCA 4127
```

```
Qy      201 ------------------------------GlnGlnAsnLysGluAspAlaTrpIle 209
                                           ||||||||||||||||||||||||||
Db     4128 TTTCTTCTTTCTTTATTTACCTTCTGGTAGGTCCAACAAAATAAAGAAGATGCCTGGATT 4187

Qy      210 GluHisAspValTrpArgMetGluIleTyrValSerLeuGlyIleValGlyLeuAlaIle 229
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4188 GAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATA 4247

Qy      230 LeuAlaLeuLeuAlaValThrSerIleProSerValSerAspSerLeuThrTrpArgGlu 249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     4248 CTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAA 4307

Qy      250 PheHisTyrIle---------------------------------------------- 253
            ||||||||||||
Db     4308 TTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTG 4367

Qy      253 ---------------------------------------------------------- 253
Db     4368 TGTTTATGATATAGAATATGTTGACTTTACCCCATAAAAAATAACAAATGTTTTTCAACA 4427

Qy      253 ---------------------------------------------------------- 253
Db     4428 GCAAAGATCTTATACTTGTTCCAATTAATAATGTGCTCTCCTGTTGTTTTCCCTATTGCT 4487

Qy      253 ---------------------------------------------------------- 253
Db     4488 TCTAATTAGGACAAGTGTTTCCTAGACATAAATAAAAGGCATTAAAATATTCTTTGTTTT 4547

Qy      253 ---------------------------------------------------------- 253
Db     4548 TTTTTTTTGTTTGTTTGTTTTTTGTTTGTTTGTTTGTTTTTTTGAGATGAAGTCTCGCTC 4607

Qy      253 ---------------------------------------------------------- 253
Db     4608 TGTTGCCCATGCTGGAGTACAGTGGCACGATCTCGGCTCACTGCAACCTGCGCCTCCTGG 4667

Qy      253 ---------------------------------------------------------- 253
Db     4668 GTTCAGGCGATTCTCTTGCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACC 4727

Qy      253 ---------------------------------------------------------- 253
Db     4728 ATGTCCAGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTTCCCATGTTGGCCAGGCTG 4787

Qy      253 ---------------------------------------------------------- 253
Db     4788 GTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATGA 4847

Qy      253 ---------------------------------------------------------- 253
Db     4848 CAGTTGTGAGCCACCACACTCAGCCTGCTCTTTCTAATATTTGAAACTTGTTAGACAATT 4907

Qy      253 ---------------------------------------------------------- 253
Db     4908 TGCCACCCATCTAATGTGATATTTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAA 4967

Qy      253 ---------------------------------------------------------- 253
Db     4968 AAAAATATTCTTTTACCTGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACTTAG 5027

Qy      253 ---------------------------------------------------------- 253
Db     5028 CACTTTCCAGAAACAAAAACTCTCTCCTTGAAATAATAGAGTTTTTATCTACCAAAGATA 5087

Qy      253 ---------------------------------------------------------- 253
Db     5088 TTCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATATACTTACTCACT 5147

Qy      253 ---------------------------------------------------------- 253
Db     5148 TGAAGTTTCTAAATATTCTTGTAATTTTAAAACTATCTCAGATTTACTGAGGTTTATCTT 5207

Qy      253 ---------------------------------------------------------- 253
Db     5208 CTGGTGGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGTCT 5267

Qy      253 ---------------------------------------------------------- 253
Db     5268 GACAAGATTCAAAGGACTAAATTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGG 5327

Qy      253 ---------------------------------------------------------- 253
Db     5328 GTAGACATCTTTGGAAATTTCCACAAGGTCAGACATTCGCAACTATCCCTTCTACATGTC 5387

Qy      253 ---------------------------------------------------------- 253
Db     5388 CACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGGAAAGTATGCCTCCATC 5447

Qy      253 ---------------------------------------------------------- 253
Db     5448 TGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCACAGAATTTCCTAATTTTG 5507

Qy      253 ---------------------------------------------------------- 253
Db     5508 TAGGTTCAGCCTGATAACCACTGGAGTTCTTTGGTCCTCATTAAATAGCTTTCTTCACAC 5567

Qy      253 ---------------------------------------------------------- 253
Db     5568 ATTGCTCTGCCTGTTACACATATGATGAACACTGCTTTTTAGACTTCATTAGGAATTTAG 5627

Qy      253 ---------------------------------------------------------- 253
Db     5628 GACTGCATCTTGACAACTGAGCCTATTCTACTATATGTACAATACCTAGCCCATAATAGG 5687

Qy      253 ---------------------------------------------------------- 253
Db     5688 TATACAATACACATTTGGTAAAACTAATTTTCAACCAATGACATGTATTTTTCAACTAGT 5747

Qy      253 ---------------------------------------------------------- 253
Db     5748 AACCTAGAAATGTTTCACTTAAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGA 5807

Qy      253 ---------------------------------------------------------- 253
Db     5808 TTCATATATGAAAACGCAAACTTAGCTATTTGATTGTATTCACTGGGACTTAAGAATGCG 5867

Qy      253 ---------------------------------------------------------- 253
Db     5868 CCTGAATAATTGTGAGTTCGATTTGTTCTGGCAGGCTAATGACCATTTCCAGTAAAGTGA 5927

Qy      253 ---------------------------------------------------------- 253
Db     5928 ATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGTTGAGATTACATAGGT 5987

Qy      253 ---------------------------------------------------------- 253
Db     5988 GAACAACTATTTTTAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGA 6047

Qy      253 ---------------------------------------------------------- 253
Db     6048 AATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATTGTTCAT 6107

Qy      253 ---------------------------------------------------------- 253
Db     6108 ATTATTTCCATGTTATCAGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCACT 6167

Qy      253 ---------------------------------------------------------- 253
Db     6168 TCATTATTCATTTATCAAAATCAGAGTGAATCACATTAGTCGCCTTCACAACTGATAAAG 6227

Qy      253 ---------------------------------------------------------- 253
Db     6228 ATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATATTTAATTGAGAA 6287

Qy      253 ---------------------------------------------------------- 253
```

```
Db       6288 TCTAAAATGTACAAATCATTGTGTTGATTCTGCAGGGATCCTGCTATAAGTAAGACTCAG 6347
Qy        253 ------------------------------------------------------------ 253
Db       6348 TCCCTGATTTTAGGTATCCTGTGATAAGCAGAATTAAGACAAATACACAAGAGACAAAGC 6407
Qy        253 ------------------------------------------------------------ 253
Db       6408 ACAAAAAATAAATATCATAAGGGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTT 6467
Qy        253 ------------------------------------------------------------ 253
Db       6468 TTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTGTTCACTTAGACAGCTTGGAGACA 6527
Qy        253 ------------------------------------------------------------ 253
Db       6528 AGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGTAGAAAGATGTGAATGG 6587
Qy        253 ------------------------------------------------------------ 253
Db       6588 ACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAG 6647
Qy        253 ------------------------------------------------------------ 253
Db       6648 CATATCCAGATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGT 6707
Qy        254 ----------GlnSerLysLeuGlyIleValSerLeuLeuLeuGlyThrIleHisAlaLe 270
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6708 TTTTCTTTTGCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATT 6767
Qy        270 uIlePheAlaTrpAsnLysTrpIleAspIleLysGlnPheValTrpTyrThrProProTh 290
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6768 GATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTCCAAC 6827
Qy        290 rPheMetIleAlaValPheLeuProIleValValLeuIlePheLysSerIleLeuPheLe 310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6828 TTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCT 6887
Qy        310 uProCysLeuArgLysLysIleLeuLysIleArgHisGlyTrpGluAspValThrLysIl 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       6888 GCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAAT 6947
Qy        330 eAsnLysThrGluIleCysSerGlnLeu 339
               |||||||||||||||||||||||||||
Db       6948 TAACAAAACTGAGATATGTTCCCAGTTG 6975

RESULT 13
US-09-439-313-342/c
; Sequence 342, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang Yuqui
;  APPLICANT:  Reed, Steven G.
;  APPLICANT:  Kalos, Michael
;  APPLICANT:  Fanger, Gary
;  APPLICANT:  Retter, Mark
;  APPLICANT:  Solk, John
;  APPLICANT:  Day, Craig
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C9
;  CURRENT APPLICATION NUMBER: US/09/439,313
;  CURRENT FILING DATE:  1999-11-12
;  NUMBER OF SEQ ID NOS: 575
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-439-313-342

Alignment Scores:
Pred. No.:                5.62e-98        Length:          592
Score:                    905.00          Matches:         171
Percent Similarity:       99.42%          Conservative:    0
Best Local Similarity:    99.42%          Mismatches:      1
Query Match:              50.56%          Indels:          0
DB:                       3               Gaps:            0

US-10-750-262-2 (1-339) x US-09-439-313-342 (1-592)

Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459
Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399
Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339
Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279
Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATAGCATCTCTGACTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219
Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159
Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 99
Qy        141 LeuHisAsnGlyThrLysTyrLysLysProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39
Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAla 172
              |||||||||  ||||||||||||||||||||||||
Db         38 AGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCT 3

RESULT 14
US-09-352-616A-342/c
; Sequence 342, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Harlocker, Susan Louise
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Mitcham, Jennifer Lynn
;  TITLE OF INVENTION:  COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF PROSTATE CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE:  210121.427C8
;  CURRENT APPLICATION NUMBER: US/09/352,616A
;  CURRENT FILING DATE:  1999-07-13
;  NUMBER OF SEQ ID NOS:  472
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-352-616A-342

Alignment Scores:
```

Pred. No.:	5.62e-98	Length:	592
Score:	905.00	Matches:	171
Percent Similarity:	99.42%	Conservative:	0
Best Local Similarity:	99.42%	Mismatches:	1
Query Match:	50.56%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-09-352-616A-342 (1-592)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 99

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAla 172
              |||||||||   |||||||||||||||||||||||||
Db         38 AGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCT 3
```

RESULT 15
US-09-636-215-342/c
; Sequence 342, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852

; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-342

Alignment Scores:

Pred. No.:	5.62e-98	Length:	592
Score:	905.00	Matches:	171
Percent Similarity:	99.42%	Conservative:	0
Best Local Similarity:	99.42%	Mismatches:	1
Query Match:	50.56%	Indels:	0
DB:	3	Gaps:	0

US-10-750-262-2 (1-339) x US-09-636-215-342 (1-592)

```
Qy          1 MetGluSerArgLysAspIleThrAsnGlnGluGluLeuTrpLysMetLysProArgArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy         21 AsnLeuGluGluAspAspTyrLeuHisLysAspThrGlyGluThrSerMetLeuLysArg 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy         41 ProValLeuLeuHisLeuHisGlnThrAlaHisAlaAspGluPheAspCysProSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy         61 LeuGlnHisThrGlnGluLeuProGlnTrpHisLeuProIleLysIleAlaAlaIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279

Qy         81 IleAlaSerLeuThrPheLeuTyrThrLeuLeuArgGluValIleHisProLeuAlaThr 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219

Qy        101 SerHisGlnGlnTyrPheTyrLysIleProIleLeuValIleAsnLysValLeuProMet 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159

Qy        121 ValSerIleThrLeuLeuAlaLeuValTyrLeuProGlyValIleAlaAlaIleValGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 99

Qy        141 LeuHisAsnGlyThrLysTyrLysLysPheProHisTrpLeuAspLysTrpMetLeuThr 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy        161 ArgLysGlnPheGlyLeuLeuSerPhePhePheAla 172
              |||||||||   |||||||||||||||||||||||||
Db         38 AGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCT 3
```

Search completed: December 6, 2005, 18:45:28
Job time : 231 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 03:12:22 ; Search time 320.456 Seconds
(without alignments)
987.688 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaaagcagaaaagacat.....ctgagatatgttcccagttg 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3289935 seqs, 155610033 residues

Total number of hits satisfying chosen parameters: 6579870

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		39.2	3.9	1779	6	US-10-750-185-25365	Sequence 25365, A
2	c	37.2	3.7	2464	6	US-10-750-185-39315	Sequence 39315, A
3		36	3.5	872	6	US-10-750-185-49060	Sequence 49060, A
4		34.2	3.4	1012	6	US-10-750-185-54610	Sequence 54610, A
5	c	34.2	3.4	3609	6	US-10-750-185-63875	Sequence 63875, A
6		34	3.3	1240	6	US-10-750-185-30880	Sequence 30880, A
7		33.8	3.3	1458	6	US-10-821-234-142	Sequence 142, App
8		33.8	3.3	2748	6	US-10-750-185-48714	Sequence 48714, A
9	c	33.4	3.3	1840	6	US-10-750-185-38532	Sequence 38532, A
10		33.2	3.3	973	6	US-10-750-185-35293	Sequence 35293, A
11	c	33.2	3.3	340000	7	US-11-102-978-3	Sequence 3, Appli
12	c	32.8	3.2	399	7	US-11-108-172-547	Sequence 547, App
13		32.8	3.2	1135	6	US-10-750-185-58068	Sequence 58068, A
14		32.8	3.2	1765	6	US-10-750-185-54184	Sequence 54184, A
15	c	32.4	3.2	1307	6	US-10-986-501-27	Sequence 27, Appl
16	c	32.4	3.2	1993	6	US-10-750-185-54772	Sequence 54772, A
17	c	32.2	3.2	1257	6	US-10-750-185-64012	Sequence 64012, A
18		32.2	3.2	1454	6	US-10-750-185-46704	Sequence 46704, A
19	c	32	3.1	1252	6	US-10-750-185-62619	Sequence 62619, A
20	c	32	3.1	3310	6	US-10-750-185-24645	Sequence 24645, A
21		32	3.1	4753	6	US-10-750-185-33545	Sequence 33545, A
22		31.8	3.1	1370	6	US-10-750-185-57153	Sequence 57153, A
23	c	31.8	3.1	1986	6	US-10-793-626-273	Sequence 273, App
24		31.8	3.1	3043	6	US-10-793-626-3478	Sequence 3478, Ap
25	c	31.8	3.1	3165	6	US-10-793-626-3360	Sequence 3360, Ap
26	c	31.8	3.1	3206	6	US-10-750-185-47856	Sequence 47856, A
27	c	31.8	3.1	3636	6	US-10-793-626-4179	Sequence 4179, Ap
28	c	31.8	3.1	4168	6	US-10-793-626-4023	Sequence 4023, Ap
29		31.6	3.1	1166	6	US-10-750-185-38045	Sequence 38045, A
30	c	31.6	3.1	1830	6	US-10-750-185-39246	Sequence 39246, A
31		31.6	3.1	1838	6	US-10-750-185-52241	Sequence 52241, A
32		31.6	3.1	3001	7	US-11-145-703-175	Sequence 175, App
33		31.6	3.1	3001	7	US-11-145-703-176	Sequence 176, App
34		31.6	3.1	150491	7	US-11-112-908-46	Sequence 46, Appl
35	c	31.4	3.1	600	6	US-10-750-185-1485	Sequence 1485, Ap
36	c	31.4	3.1	1407	6	US-10-750-185-44414	Sequence 44414, A
37	c	31.4	3.1	1637	6	US-10-750-185-26752	Sequence 26752, A
38	c	31.4	3.1	2205	6	US-10-750-185-27481	Sequence 27481, A
39	c	31.4	3.1	4176	6	US-10-793-626-4262	Sequence 4262, Ap
40		31.4	3.1	149419	7	US-11-112-908-49	Sequence 49, Appl
41		31.4	3.1	166111	7	US-11-112-908-47	Sequence 47, Appl
42		31.2	3.1	1123	6	US-10-750-185-54609	Sequence 54609, A
43		31.2	3.1	1621	6	US-10-750-185-63586	Sequence 63586, A
44	c	31.2	3.1	2988	6	US-10-750-185-30138	Sequence 30138, A
45	c	31.2	3.1	3194	6	US-10-750-185-48072	Sequence 48072, A

ALIGNMENTS

RESULT 1
US-10-750-185-25365
; Sequence 25365, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DeNISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMI1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 25365
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Bovine 19866880604913
US-10-750-185-25365

Query Match 3.9%; Score 39.2; DB 6; Length 1779;
Best Local Similarity 54.1%; Pred. No. 0.1;
Matches 80; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```
Qy        704 TGACATCTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGA 763
              ||||||  ||||  ||||| | ||    | | || || |  |  ||| | |||||    |
Db        765 TGACATTAATTCTGTCTGTTACTGTTATTCTTACTTGTATCGGGTTTAATTATATCATTA 824

Qy        764 GCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGA 823
                ||||      |   ||   ||| | ||| ||| |  | |   | |||||| | | | |
Db        825 AAAAGCACATGACACTTAGTCTTTTGCTGTGCAAATAAGATAAAATGATTTGTCCTTTGT 884

Qy        824 ATAAGTGGATAGATATAAAACAATTTGT 851
                | |  ||    | ||| | ||||
Db        885 TAACTTATATTTTAAAAAACAATGTTGT 912
```

RESULT 2
US-10-750-185-39315/c
; Sequence 39315, Application US/10750185

```
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 39315
;   LENGTH: 2464
;   TYPE: DNA
;   ORGANISM: Bovine  19866881564211
US-10-750-185-39315

  Query Match             3.7%;  Score 37.2;  DB 6;  Length 2464;
  Best Local Similarity   50.6%;  Pred. No. 0.48;
  Matches   90;  Conservative    0;  Mismatches   88;  Indels    0;  Gaps    0;

Qy        834 AGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCC 893
              ||| | |    || || |    |||| |   |||   |  |  ||| |||   ||
Db       1748 AGAGAAAGGGAAAATTCTGGAATATAAAATGCCATTCTGCAGTATATCTGCAGTCTCAAT 1689

Qy        894 AATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACT 953
              ||  |    | ||| ||||     | | ||  ||||   |    | | |||||| | |
Db       1688 AACAGCAAGCATGAAATTTGTTCTCTTCCTTGTCCTATTAATAGTTAAGAAGAACAAAGA 1629

Qy        954 GAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCC 1011
              |||||   | | |   |  ||||  |||  ||||  |  || |   | || | ||||
Db       1628 CAAGATGTTAAACGTGGGTAAAGAAATCATTAAAAAAACAAACAAACACATGTTTTCC 1571


RESULT 3
US-10-750-185-49060
; Sequence 49060, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 49060
;   LENGTH: 872
;   TYPE: DNA
;   ORGANISM: Bovine  19866881284640
US-10-750-185-49060

  Query Match             3.5%;  Score 36;  DB 6;  Length 872;
  Best Local Similarity   51.9%;  Pred. No. 0.61;
  Matches   81;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy        316 TTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTC 375
              | || |   || |  | ||    || |  |||| |||| || ||  ||    ||| |
Db         57 TATTCTCTTATCCACAACCCCACCACCTCCAAACTCTTTCCCATATTTATTTTCATTGGG 116

Qy        376 TTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACC 435
              ||    |  ||| ||   |    ||||    || || | |  |  ||  ||| | ||||
Db        117 TTTATTTCCATTTTCCATACTCCAGTGACTATAGTAAATTTTGAGATTTGTAAGGTAACC 176

Qy        436 AAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGG 471
              ||  || ||||| ||    | || |     |  ||||
Db        177 AAAAATGAGAAGGTTGGGAAATGCTCTATTGCGTGG 212


RESULT 4
US-10-750-185-54610
; Sequence 54610, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 54610
;   LENGTH: 1012
;   TYPE: DNA
;   ORGANISM: Bovine  19866881259787
US-10-750-185-54610

  Query Match             3.4%;  Score 34.2;  DB 6;  Length 1012;
  Best Local Similarity   54.3%;  Pred. No. 2.2;
  Matches   69;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy        235 GCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTA 294
              || | || | || | |    |||  |||| |||    | || |   ||  |   | |||
Db        237 GCAAATAAACCACCACAACATTTCTTTTATACTTCAGTTAGAGTGTTACATTGACTTTTT 296

Qy        295 GCAACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTG 354
              || ||   || ||  |||||||   | | || || |   ||  || || ||   | |
Db        297 AAAAATTTAGATGAATTATATTTTGTAAGAGTTTCACTTAAGGAGATAAAAAAGAGCATC 356

Qy        355 CCAATGG 361
              |||||||
Db        357 ACAATGG 363


RESULT 5
US-10-750-185-63875/c
; Sequence 63875, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
```

```
; SEQ ID NO 63875
;   LENGTH: 3609
;   TYPE: DNA
;   ORGANISM: Bovine  19866880579152
US-10-750-185-63875

  Query Match             3.4%;  Score 34.2;  DB 6;  Length 3609;
  Best Local Similarity   58.3%;  Pred. No. 4.5;
  Matches   60;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy        237 TATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGC 296
              |||| ||||| | | |  || ||| ||| |||| | ||   |  | || |    |
Db       1979 TATTTAAGCATTTTTCAAATTACTTCACAGTCTTTTAAGATCATCATTTAATTGCTGCAT 1920

Qy        297 AACTTCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTC 339
              ||| | |||| || || || ||| |||  | |  |  |  |||
Db       1919 AACATTCCATGAAGAAAATGTTTTTAACTTACATAAGCATGTC 1877


RESULT 6
US-10-750-185-30880
; Sequence 30880, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 30880
;   LENGTH: 1240
;   TYPE: DNA
;   ORGANISM: Bovine  19866881208716
US-10-750-185-30880

  Query Match             3.3%;  Score 34;  DB 6;  Length 1240;
  Best Local Similarity   46.9%;  Pred. No. 2.9;
  Matches  106;  Conservative    0;  Mismatches  120;  Indels    0;  Gaps    0;

Qy        125 TGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTC 184
              |||| ||||   |||      |  |      |   ||| | ||   | ||       ||| |
Db        301 TGCTGTTGCTGCTGCTAAGTTCTTCAGTCGTGTCTGACTCTGTGCGACCCCATAGACTGC 360

Qy        185 AGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAG 244
              ||| |||   |   | | | | ||  ||  |||| || |  |  |            | |
Db        361 AGCCCACCAGGCTCCCCATCCTACTTTGCTACTTCCCCAGAATTAAGCTATAGCACAGAA 420

Qy        245 CATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCC 304
              |   ||| |  || || |    || |     |||| || |      ||  | |||||  |
Db        421 CCAACCTGTCCATTTTTCATGTCCTCCATTCTGAAGCAACTGCTGTTTCTGAAACTTTTC 480

Qy        305 ATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGT 350
              |    ||  | | ||  |   || |||  |  ||  ||||| |||
Db        481 AATTGCATCAATATTCCATTTCTCAAATATTTATCTACAACACAGT 526


RESULT 7
US-10-821-234-142
; Sequence 142, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
;  APPLICANT: Labat, Ivan
;  APPLICANT:  Stache-Crain, Birgit
;  APPLICANT:  Andarmani, Susan
;  APPLICANT:  Tang, Y. Tom
;  TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
;  FILE REFERENCE: 821A
;  CURRENT APPLICATION NUMBER: US/10/821,234
;  CURRENT FILING DATE:  2004-04-07
;  PRIOR APPLICATION NUMBER: US 60/462,047
;  PRIOR FILING DATE: 2003-04-07
;  NUMBER OF SEQ ID NOS: 1704
;  SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 142
;   LENGTH: 1458
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-821-234-142

  Query Match             3.3%;  Score 33.8;  DB 6;  Length 1458;
  Best Local Similarity   47.1%;  Pred. No. 3.6;
  Matches  104;  Conservative    0;  Mismatches  117;  Indels    0;  Gaps    0;

Qy         12 AAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATTTAGAAGA 71
              || |  ||   |  |  |||  ||  | | |||   |  | ||  ||| |       | ||
Db        287 AAGACGCAAGTCCCATGAAGCTGAGGTCTTGAAGCAGCTGGCTGAGAAACGAGAGCACGA 346

Qy         72 AGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTT 131
                | ||     | || ||||  |  | ||||| || ||   | |  | | |      |
Db        347 GAAAGAAGTGCTTCAGAAGGCAATAGAAGAGAACAACAACTTCAGTAAAATGGCAGAAGA 406

Qy        132 GCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACAC 191
              | |  ||  ||| | |     | ||| || ||     || |      || || |      ||
Db        407 GAAACTGACCCACAAAATGGAAGCTAATAAAGAGAACCGAGAGGCACAAATGGCTGCCAA 466

Qy        192 ACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAG 232
              || |||||  || | | ||  | |   ||  ||| ||  ||
Db        467 ACTGGAACGTTTGCGAGAGAAGGATAAGCACATTGAAGAAG 507


RESULT 8
US-10-750-185-48714
; Sequence 48714, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48714
;   LENGTH: 2748
;   TYPE: DNA
;   ORGANISM: Bovine  19866880696598
US-10-750-185-48714

  Query Match             3.3%;  Score 33.8;  DB 6;  Length 2748;
  Best Local Similarity   57.7%;  Pred. No. 5;
  Matches   79;  Conservative    0;  Mismatches   57;  Indels    1;  Gaps    1;

Qy        789 ACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATT 848
              |||||  | |  ||| |||||  | ||| ||| || |   |  |  ||  | || | |||
Db        666 ACTGGATAGATGACATGCATTCTTCTTTCCCTTGACTCTCTCTAATGAGCTTAAGC-ATT 724

Qy        849 TGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGAT 908
              ||||||| ||    || ||| |   |||||||  | |       | || | | |     ||
```

```
Db        725 TGTATGGCATTTGTCTACAATTAGCATGATAGTAGGTGATACGCTAAATCTGGGGTAAAT 784

Qy        909 ATTTAAAAGCATACTAT 925
              | ||||| || | | |
Db        785 TTCTAAAACCAAAATCT 801


RESULT 9
US-10-750-185-38532/c
; Sequence 38532, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 38532
;   LENGTH: 1840
;   TYPE: DNA
;   ORGANISM: Bovine  19866881352831
US-10-750-185-38532

  Query Match             3.3%;  Score 33.4;  DB 6;  Length 1840;
  Best Local Similarity   58.6%;  Pred. No. 5.3;
  Matches   58;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy        836 ATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAA 895
              |||   || | | | | || | |  || |  |||||||  |   || ||||  |||  |
Db       1252 ATAATGAAAATTGTATTTGCTTTTGACTTATAACTTTTAATACCTCTTTTTTTTTTCAGA 1193

Qy        896 TTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCAT 934
              |   | | || |  ||| |||| ||   |||  ||| ||
Db       1192 TATCTTTGCTTAACTTTCAAAGAATCAGATTAATGCAAT 1154


RESULT 10
US-10-750-185-35293
; Sequence 35293, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 35293
;   LENGTH: 973
;   TYPE: DNA
;   ORGANISM: Bovine  19866881541753
US-10-750-185-35293

  Query Match             3.3%;  Score 33.2;  DB 6;  Length 973;
  Best Local Similarity   57.8%;  Pred. No. 4.3;
  Matches   59;  Conservative    0;  Mismatches   43;  Indels    0;  Gaps    0;

Qy        870 TTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCT 929
              ||||  | | ||||   || |  |  || ||| |  | |       |||| ||| ||  ||
Db        844 TTTTTTAACAGCTTGGTTACAGCTCATAGTTTTATTCAGTAAACAAAGGATAGTACACCC 903

Qy        930 GCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTG 971
              ||| || |||||  | |||| |  |||   || | ||  ||
Db        904 CCCAGGCGTGAGGGTGGAGATCCCAAAGGAGAGGCCTGTATG 945


RESULT 11
US-11-102-978-3/c
; Sequence 3, Application US/11102978
; Publication No. US20050250142A1
; GENERAL INFORMATION:
;  APPLICANT: University of Utah Technology Transfer Office
;  APPLICANT:  University of Utah Research Foundation
;  TITLE OF INVENTION: Diagnosis and Treatment of Herpes Simplex Virus Disease
;  FILE REFERENCE: 0274-5537.1US
;  CURRENT APPLICATION NUMBER: US/11/102,978
;  CURRENT FILING DATE:  2005-04-11
;  PRIOR APPLICATION NUMBER: PCT/US2003/033152
;  PRIOR FILING DATE: 2003-10-18
;  PRIOR APPLICATION NUMBER: 60/419,576
;  PRIOR FILING DATE: 2002-10-18
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
;   LENGTH: 340000
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (56948)..(57115)
;   OTHER INFORMATION: C21orf34 exon
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (80006)..(81089)
;   OTHER INFORMATION: Gene VDAC2P; voltage-dependent anion channel isoform 2 pseudogene
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (167308)..(167438)
;   OTHER INFORMATION: C21orf34 exon
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: (216732)..(216833)
;   OTHER INFORMATION: C21orf34 exon
US-11-102-978-3

  Query Match             3.3%;  Score 33.2;  DB 7;  Length 340000;
  Best Local Similarity   52.1%;  Pred. No. 98;
  Matches   74;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        746 AATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCACAATACACG 805
              ||||    |||  |  |  |||| ||   | | |   |||| || ||| || ||  |||
Db       9668 AATTAAGATATCATAGGTTCAAGTTACACAATTTACACCTTTTATTGGTCATAAGTCACA 9609

Qy        806 CATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTATACACCTC 865
              || |   | |       | | |  || |||  ||||| |    |||    ||| |||
Db       9608 CAGTAGCATATTTTATTTGTCATTTAATTGATTCAAAACCAAAAATATATGTTACCCCTT 9549

Qy        866 CAACTTTTATGATAGCTGTTTT 887
              | | |  || |  || | || |
Db       9548 CTATTGCTAAGCCAGGTATTAT 9527


RESULT 12
US-11-108-172-547/c
; Sequence 547, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Lodes, Michael J.
;  APPLICANT:  Secrist, Heather
;  APPLICANT:  Benson, Darin R.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Wang, Tongtong
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Smith, Carole L.
;  APPLICANT:  King, Gordon E.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Clapper, Jonathan D.
;  APPLICANT:  Skeiky, Yasir A. W.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Vedvick Thomas S.
;  APPLICANT:  Carter, Darrick
;  TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
;  TITLE OF INVENTION:  OF COLON CANCER AND METHODS FOR THEIR USE
;  FILE REFERENCE: 210121.471C15
;  CURRENT APPLICATION NUMBER: US/11/108,172
;  CURRENT FILING DATE:  2005-04-15
;  PRIOR APPLICATION NUMBER: US 10/025,380
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 09/922,217
;  PRIOR FILING DATE: 2001-08-03
;  PRIOR APPLICATION NUMBER: US 09/833,263
;  PRIOR FILING DATE: 2001-04-10
;  PRIOR APPLICATION NUMBER: US 09/649,811
;  PRIOR FILING DATE: 2000-08-28
;  PRIOR APPLICATION NUMBER: US 09/609,448
;  PRIOR FILING DATE: 2000-06-29
;  PRIOR APPLICATION NUMBER: US 09/575,251
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: US 09/519,444
;  PRIOR FILING DATE: 2000-03-06
;  PRIOR APPLICATION NUMBER: US 09/504,629
;  PRIOR FILING DATE: 2000-02-15
;  PRIOR APPLICATION NUMBER: US 09/480,321
;  PRIOR FILING DATE: 2000-01-10
;  PRIOR APPLICATION NUMBER: US 09/476,296
;  PRIOR FILING DATE: 1999-12-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1130
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 547
;   LENGTH: 399
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-11-108-172-547

  Query Match             3.2%;  Score 32.8;  DB 7;  Length 399;
  Best Local Similarity   55.8%;  Pred. No. 3.5;
  Matches   58;  Conservative    2;  Mismatches   44;  Indels    0;  Gaps    0;

Qy          5 AAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGAAATT 64
              |||| | ||| |  || |   |  |||| || ||||| ||||  | |       |||
Db        115 AAAGTAAAAATGTAATAATTGAAATAGAAAAAGTTTGGTAAATTCAACACCTACGAATGA 56

Qy         65 TAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGC 108
              ||||| |  | ||:  :|   | ||| | ||    ||||| ||
Db         55 TAGAACACCAAGAWRTYTATTAGAAGAAAACTTTGAGACCTGC 12


RESULT 13
US-10-750-185-58068
; Sequence 58068, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 58068
;   LENGTH: 1135
;   TYPE: DNA
;   ORGANISM: Bovine  19866881974092
US-10-750-185-58068

  Query Match             3.2%;  Score 32.8;  DB 6;  Length 1135;
  Best Local Similarity   64.5%;  Pred. No. 6.1;
  Matches   49;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        443 AGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCA 502
              | ||  || ||||||   |    ||  | | |  |||||||||  | |||| | || | |
Db        314 ATAAACTTTCACATTTCATCATCAAAGGAAAGGCAACAAGAAAATATTTTGTGTTTGTTA 373

Qy        503 GTTTCTTTTTTGCTGT 518
              ||||||||||| | |
Db        374 GTTTCTTTTTTTTTT 389


RESULT 14
US-10-750-185-54184
; Sequence 54184, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
;  APPLICANT: MMI GENOMICS, INC.
;  APPLICANT:  DeNISE, Sue K.
;  APPLICANT:  KERR, Richard
;  APPLICANT:  ROSENFELD, David
;  APPLICANT:  HOLM, Tom
;  APPLICANT:  BATES, Stephen
;  APPLICANT:  FANTIN, Dennis
;  TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
;  FILE REFERENCE: MMI1100-2
;  CURRENT APPLICATION NUMBER: US/10/750,185
;  CURRENT FILING DATE:  2003-12-31
;  PRIOR APPLICATION NUMBER: US 60/437,482
;  PRIOR FILING DATE: 2002-12-31
;  NUMBER OF SEQ ID NOS: 64922
;  SOFTWARE: PatentIN version 3.1
; SEQ ID NO 54184
;   LENGTH: 1765
;   TYPE: DNA
;   ORGANISM: Bovine  19866880384477
US-10-750-185-54184

  Query Match             3.2%;  Score 32.8;  DB 6;  Length 1765;
  Best Local Similarity   64.5%;  Pred. No. 7.8;
  Matches   49;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        479 CAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTC 538
              |||| ||  | ||||   ||||||  | ||| |||||| | |||||||| |   | |||
Db         45 CAAGTAAATATTTTGAAGTTCTCATCTACTTCTTTGCTTTTCTGCATGCCAAGGACAGTG 104

Qy        539 TGTCTTACCCAATGAG 554
              || |   |   || ||
Db        105 TGGCCCCCTGCATAAG 120


RESULT 15
US-10-986-501-27/c
; Sequence 27, Application US/10986501
; Publication No. US20050244845A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: 90 Human Secreted Proteins
;  FILE REFERENCE: PZ013P2C1
;  CURRENT APPLICATION NUMBER: US/10/986,501
;  CURRENT FILING DATE:  2004-11-12
;  PRIOR APPLICATION NUMBER: US/10/621,363
;  PRIOR FILING DATE: 2003-07-18
;  PRIOR APPLICATION NUMBER: 09/969,730
;  PRIOR FILING DATE: 2001-10-06
;  PRIOR APPLICATION NUMBER: 09/774,639
;  PRIOR FILING DATE: 2001-02-01
;  PRIOR APPLICATION NUMBER: 60/238,291
;  PRIOR FILING DATE: 2000-10-06
;  PRIOR APPLICATION NUMBER: 09/244,112
;  PRIOR FILING DATE: 1999-02-04
;  PRIOR APPLICATION NUMBER: PCT/US98/16235
;  PRIOR FILING DATE: 1998-08-04
;  PRIOR APPLICATION NUMBER: 60/056,371
;  PRIOR FILING DATE: 1997-08-19
;  PRIOR APPLICATION NUMBER: 60/056,732
;  PRIOR FILING DATE: 1997-08-19
;  PRIOR APPLICATION NUMBER: 60/056,366
;  PRIOR FILING DATE: 1997-08-19
;  PRIOR APPLICATION NUMBER: 60/056,364
;  PRIOR FILING DATE: 1997-08-19
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 373
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
;   LENGTH: 1307
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-986-501-27

  Query Match             3.2%;  Score 32.4;  DB 6;  Length 1307;
  Best Local Similarity   50.5%;  Pred. No. 8.7;
  Matches  111;  Conservative    0;  Mismatches  101;  Indels    8;  Gaps    1;

Qy        590 ATCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGG 649
              ||| ||||||    ||||||  ||||||   |  |||||| |    || ||    ||
Db        573 ATCCACAGGTGTGGCAAAATGGAGAAGACCTCCTGATTGAACTGATTGATTTATAAACCA 514

Qy        650 AGATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACAT 709
              ||| |  ||| | ||   |||   |   | |   || |   ||| |         ||||
Db        513 AGAATGGTGTTTTTCCTTGAAAACTTTTACTTCAAACAGCTGCTGTA--------GACAC 462

Qy        710 CTATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGC 769
               ||||  |   || | || ||| ||  | || | ||   || || |  || | |   |
Db        461 ATATTGAACAAGTAAATGGCTCCTTCTCCTGAACAGGGGTTAACCAGTTTTACAAACATT 402

Qy        770 TAGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATT 809
                ||| ||   |||||     |||   |  |   |||
Db        401 AGCCCATTTTTCATCTTCTTTGAAGCATCTTTTAAATATT 362


Search completed: December  5, 2005, 08:05:52
Job time : 323.456 secs
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 5, 2005, 00:23:57 ; Search time 949.415 Seconds
(without alignments)
8858.046 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaaagcagaaaagacat.....ctgagatatgttcccagttg 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1017	100.0	1177	8	US-10-696-639-15	Sequence 15, Appl
2	1017	100.0	1193	6	US-10-165-044-1	Sequence 1, Appli
3	1017	100.0	1193	7	US-10-408-009-1	Sequence 1, Appli
4	1017	100.0	1193	8	US-10-857-785-1	Sequence 1, Appli
5	1017	100.0	1193	8	US-10-856-109-1	Sequence 1, Appli
6	1017	100.0	1193	8	US-10-830-899-2	Sequence 2, Appli
7	1017	100.0	1193	8	US-10-753-195-1	Sequence 1, Appli
8	1017	100.0	1193	9	US-10-752-421-1	Sequence 1, Appli
9	1017	100.0	1193	9	US-10-861-662-2	Sequence 2, Appli
10	1017	100.0	1195	3	US-09-759-143-878	Sequence 878, App
11	1017	100.0	1195	3	US-09-780-669-878	Sequence 878, App
12	1017	100.0	1195	3	US-09-822-827-878	Sequence 878, App
13	1017	100.0	1195	3	US-09-895-793-878	Sequence 878, App
14	1017	100.0	1195	3	US-09-895-814-878	Sequence 878, App
15	1017	100.0	1195	5	US-10-012-896-878	Sequence 878, App
16	1017	100.0	1195	5	US-10-011-095-1	Sequence 1, Appli
17	1017	100.0	1195	5	US-10-010-667A-1	Sequence 1, Appli
18	1017	100.0	1195	5	US-10-205-823-396	Sequence 396, App
19	1017	100.0	1195	6	US-10-144-678A-878	Sequence 878, App
20	1017	100.0	1195	6	US-10-294-025-878	Sequence 878, App
21	1017	100.0	1195	6	US-10-393-590-35	Sequence 35, Appl
22	1017	100.0	1195	6	US-10-393-567-35	Sequence 35, Appl
23	1017	100.0	1195	6	US-10-394-087-35	Sequence 35, Appl
24	1017	100.0	1195	6	US-10-295-027-713	Sequence 713, App
25	1017	100.0	1195	6	US-10-295-027-1130	Sequence 1130, Ap
26	1017	100.0	1195	8	US-10-643-795A-16	Sequence 16, Appl
27	1017	100.0	1195	8	US-10-643-795A-42	Sequence 42, Appl
28	1017	100.0	1195	9	US-10-750-262-1	Sequence 1, Appli
29	1017	100.0	1195	9	US-10-948-518-16	Sequence 16, Appl
30	1017	100.0	1195	9	US-10-948-518-42	Sequence 42, Appl
31	1017	100.0	1195	9	US-10-956-157-1811	Sequence 1811, Ap
32	1017	100.0	1195	9	US-10-956-157-7046	Sequence 7046, Ap
33	1017	100.0	1195	9	US-10-858-887-1	Sequence 1, Appli
34	1017	100.0	1195	9	US-10-631-467-428	Sequence 428, App
35	1017	100.0	1195	10	US-11-051-454-396	Sequence 396, App
36	1017	100.0	1201	7	US-10-425-114-16445	Sequence 16445, A
37	1017	100.0	1277	3	US-09-814-353-19910	Sequence 19910, A
38	1017	100.0	1330	7	US-10-755-889-191	Sequence 191, App
39	988	97.1	1354	8	US-10-723-860-5120	Sequence 5120, Ap
40	870	85.5	1365	8	US-10-830-899-6	Sequence 6, Appli
41	870	85.5	1365	9	US-10-861-662-6	Sequence 6, Appli
42	762.2	74.9	3627	8	US-10-830-899-10	Sequence 10, Appl
43	762.2	74.9	3627	9	US-10-861-662-10	Sequence 10, Appl
44	760.6	74.8	3627	5	US-10-011-095-6	Sequence 6, Appli
45	760.6	74.8	3627	5	US-10-010-667A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-696-639-15
; Sequence 15, Application US/10696639
; Publication No. US20050037439A1
; GENERAL INFORMATION:
; APPLICANT: Pharmacia Corporation
; APPLICANT: Bourner, Maureen J.
; TITLE OF INVENTION: DIFERENTIALLY EXPRESSED GENES INVOLVED IN CANCER, THE
; TITLE OF INVENTION: POLYPEPTIDES ENCODED THEREBY, AND METHODS OF USING THE SAME
; FILE REFERENCE: 01040/1
; CURRENT APPLICATION NUMBER: US/10/696,639
; CURRENT FILING DATE: 2003-10-29
; PRIOR APPLICATION NUMBER: 60/422,176
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 3114
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-696-639-15

Query Match 100.0%; Score 1017; DB 8; Length 1177;
Best Local Similarity 100.0%; Pred. No. 6.9e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365
```

```
Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 2
US-10-165-044-1
; Sequence 1, Application US/10165044
; Publication No. US20030149531A1
; GENERAL INFORMATION:
; APPLICANT: Agensys, Inc.
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas Saffran
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Steven Chappell Mitchell
; APPLICANT: Mary Faris
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 51158-20016.02
; CURRENT APPLICATION NUMBER: US/10/165,044
; CURRENT FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: US 60/091,183
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/455,486
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: WO 99/62941
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: PCT/US00/33040
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1191)
US-10-165-044-1

Query Match 100.0%; Score 1017; DB 6; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843
```

```
Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 3
US-10-408-009-1
; Sequence 1, Application US/10408009
; Publication No. US20040072196A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001603
;  CURRENT APPLICATION NUMBER: US/10/408,009
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  NUMBER OF SEQ ID NOS: 36
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-408-009-1

  Query Match             100.0%;  Score 1017;  DB 7;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 7e-277;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 4
US-10-857-785-1
; Sequence 1, Application US/10857785
; Publication No. US20040219162A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001607
;  CURRENT APPLICATION NUMBER: US/10/857,785
;  CURRENT FILING DATE:  2004-05-28
;  PRIOR APPLICATION NUMBER: US 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: US 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: US 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: US 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
```

```
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-857-785-1

  Query Match            100.0%;  Score 1017;  DB 8;  Length 1193;
  Best Local Similarity  100.0%;  Pred. No. 7e-277;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 5
US-10-856-109-1
; Sequence 1, Application US/10856109
; Publication No. US20040219591A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001606
;  CURRENT APPLICATION NUMBER: US/10/856,109
;  CURRENT FILING DATE:  2004-05-28
;  PRIOR APPLICATION NUMBER: US 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: US 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: US 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: US 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-856-109-1

  Query Match            100.0%;  Score 1017;  DB 8;  Length 1193;
  Best Local Similarity  100.0%;  Pred. No. 7e-277;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483
```

```
Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 6
US-10-830-899-2
; Sequence 2, Application US/10830899
; Publication No. US20040253232A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Etessami, Soudabeh
;  APPLICANT:  Challita-Eid, Pia M.
;  APPLICANT:  Perez-Villar, Juan
;  APPLICANT:  Meyrick Morrison, Karen Jane
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Faris, Mary
;  APPLICANT:  Gudas, Jean
;  APPLICANT:  Raitano, Arthur B.
;  TITLE OF INVENTION: Antibodies and Molecules Derived
;  TITLE OF INVENTION:  therefrom that Bind to STEAP-1 Proteins
;  FILE REFERENCE: 51158-20016.26
;  CURRENT APPLICATION NUMBER: US/10/830,899
;  CURRENT FILING DATE:  2004-04-23
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: 10/010,667
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 10/011,095
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 10/236,878
;  PRIOR FILING DATE: 2002-09-06
;  PRIOR APPLICATION NUMBER: 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;  LENGTH: 1193
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (66)...(1085)
US-10-830-899-2

  Query Match             100.0%;  Score 1017;  DB 8;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 7e-277;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 7
US-10-753-195-1
; Sequence 1, Application US/10753195
; Publication No. US20050004349A1
; GENERAL INFORMATION:
;  APPLICANT: Agensys, Inc.
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas Saffran
;  APPLICANT:  Daniel E.H. Afar
;  APPLICANT:  Steven Chappell Mitchell
;  APPLICANT:  Mary Faris
;  APPLICANT:  Aya Jakobovits
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 51158-20016.02
;  CURRENT APPLICATION NUMBER: US/10/753,195
;  CURRENT FILING DATE:  2004-01-06
;  PRIOR APPLICATION NUMBER: US/10/165,044
;  PRIOR FILING DATE: 2002-06-06
;  PRIOR APPLICATION NUMBER: US 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: US 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  PRIOR APPLICATION NUMBER: US 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: US 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: WO 99/62941
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: PCT/US00/33040
;  PRIOR FILING DATE: 2000-12-06
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1191)
US-10-753-195-1

  Query Match             100.0%;  Score 1017;  DB 8;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 7e-277;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 8
US-10-752-421-1
; Sequence 1, Application US/10752421
; Publication No. US20050063975A1
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Stephen C. Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 511582001612
;  CURRENT APPLICATION NUMBER: US/10/752,421
;  CURRENT FILING DATE:  2004-01-05
;  PRIOR APPLICATION NUMBER: US 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: US 09/323,873
;  PRIOR FILING DATE: 1999-06-01
```

```
;  PRIOR APPLICATION NUMBER: US 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: US 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (64)...(1083)
US-10-752-421-1
```

Query Match 100.0%; Score 1017; DB 9; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

```
RESULT 9
US-10-861-662-2
; Sequence 2, Application US/10861662
; Publication No. US20050086707A1
; GENERAL INFORMATION:
;  APPLICANT: Jakobovits, Aya
;  APPLICANT:  Etessami, Soudabeh
;  APPLICANT:  Challita-Eid, Pia M.
;  APPLICANT:  Perez-Villar, Juan
;  APPLICANT:  Meyrick Morrison, Karen Jane
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Faris, Mary
;  APPLICANT:  Gudas, Jean
;  APPLICANT:  Raitano, Arthur B.
;  TITLE OF INVENTION: Antibodies and Molecules Derived
;  TITLE OF INVENTION:  therefrom that Bind to STEAP-1 Proteins
;  FILE REFERENCE: 51158-20016.26
;  CURRENT APPLICATION NUMBER: US/10/861,662
;  CURRENT FILING DATE:  2004-06-04
;  PRIOR APPLICATION NUMBER: 09/323,873
;  PRIOR FILING DATE: 1999-06-01
;  PRIOR APPLICATION NUMBER: 10/010,667
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 10/011,095
;  PRIOR FILING DATE: 2001-12-06
;  PRIOR APPLICATION NUMBER: 10/236,878
;  PRIOR FILING DATE: 2002-09-06
;  PRIOR APPLICATION NUMBER: 09/455,486
;  PRIOR FILING DATE: 1999-12-06
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 103
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1193
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (66)...(1085)
US-10-861-662-2
```

Query Match 100.0%; Score 1017; DB 9; Length 1193;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245
```

```
Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 10
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. US20020022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C23
; CURRENT APPLICATION NUMBER: US/09/759,143
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 934
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-759-143-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 11
US-09-780-669-878
; Sequence 878, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C24
;  CURRENT APPLICATION NUMBER: US/09/780,669
;  CURRENT FILING DATE:  2001-02-09
;  NUMBER OF SEQ ID NOS:  943
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-780-669-878

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 7e-277;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 12
US-09-822-827-878
; Sequence 878, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.534C1
;  CURRENT APPLICATION NUMBER: US/09/822,827
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 982
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
```

; ORGANISM: Homo sapiens
US-09-822-827-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 13
US-09-895-793-878
; Sequence 878, Application US/09895793
; Publication No. US20020192763A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.534C2
; CURRENT APPLICATION NUMBER: US/09/895,793
; CURRENT FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-895-793-878

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

```
RESULT 14
US-09-895-814-878
; Sequence 878, Application US/09895814
; Publication No. US20020193296A1
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C26
;  CURRENT APPLICATION NUMBER: US/09/895,814
;  CURRENT FILING DATE:  2001-06-29
;  NUMBER OF SEQ ID NOS: 990
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-895-814-878

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 7e-277;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965
```

```
Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 15
US-10-012-896-878
; Sequence 878, Application US/10012896
; Publication No. US20020183251A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Kalos, Michael D.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Hural, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Vinals de Bassols, Carlota
; APPLICANT: Foy, Teresa
; APPLICANT: Fanger, Gary R.
; APPLICANT: Wantanabe, Yoshihiro
; APPLICANT: Meagher, Madeleine Joy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C27
; CURRENT APPLICATION NUMBER: US/10/012,896
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 1011
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-012-896-878

Query Match 100.0%; Score 1017; DB 5; Length 1195;
Best Local Similarity 100.0%; Pred. No. 7e-277;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

Search completed: December 5, 2005, 07:54:11
Job time : 952.415 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:43:36 ; Search time 202.756 Seconds
(without alignments)
8916.024 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaaagcagaaaagacat.....ctgagatatgttcccagttg 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1017	100.0	1193	3	US-09-455-486-1	Sequence 1, Appli
	2	1017	100.0	1195	3	US-09-323-873A-1	Sequence 1, Appli
	3	1017	100.0	1195	3	US-09-685-166A-878	Sequence 878, App
	4	1017	100.0	1195	3	US-09-679-426-878	Sequence 878, App
	5	1017	100.0	1195	3	US-09-759-143-878	Sequence 878, App
	6	1017	100.0	1195	3	US-10-010-667A-1	Sequence 1, Appli
	7	1017	100.0	1195	3	US-10-012-896-878	Sequence 878, App
	8	1015.4	99.8	1147	3	US-09-949-016-2686	Sequence 2686, Ap
	9	760.6	74.8	3627	3	US-09-323-873A-6	Sequence 6, Appli
	10	760.6	74.8	3627	3	US-09-455-486-4	Sequence 4, Appli
	11	760.6	74.8	3627	3	US-10-010-667A-6	Sequence 6, Appli
c	12	516	50.7	592	3	US-09-439-313-342	Sequence 342, App
c	13	516	50.7	592	3	US-09-352-616A-342	Sequence 342, App
c	14	516	50.7	592	3	US-09-636-215-342	Sequence 342, App
c	15	516	50.7	592	3	US-09-685-166A-342	Sequence 342, App
c	16	516	50.7	592	3	US-09-679-426-342	Sequence 342, App
c	17	516	50.7	592	3	US-09-759-143-342	Sequence 342, App
c	18	516	50.7	592	3	US-09-651-236-342	Sequence 342, App
c	19	516	50.7	592	3	US-09-657-279-342	Sequence 342, App
c	20	516	50.7	592	3	US-10-012-896-342	Sequence 342, App
	21	515.6	50.7	9073	3	US-09-949-016-14428	Sequence 14428, A
	22	266.6	26.2	2453	3	US-09-455-486-5	Sequence 5, Appli
	23	266.6	26.2	2469	3	US-10-104-047-1185	Sequence 1185, Ap
	24	265	26.1	1403	3	US-10-012-896-995	Sequence 995, App
	25	256.8	25.3	455	3	US-09-621-976-9264	Sequence 9264, Ap
c	26	229.6	22.6	848	3	US-10-012-896-993	Sequence 993, App
	27	221.4	21.8	519	3	US-10-010-667A-7	Sequence 7, Appli
	28	221.4	21.8	521	3	US-09-323-873A-7	Sequence 7, Appli
	29	212.8	20.9	2714	3	US-09-562-930-5	Sequence 5, Appli
	30	212.8	20.9	3884	3	US-09-562-930-10	Sequence 10, Appl
	31	187.4	18.4	4429	3	US-09-455-486-7	Sequence 7, Appli
	32	184.8	18.2	1213	3	US-09-083-521-3	Sequence 3, Appli
	33	171	16.8	1886	3	US-09-562-930-1	Sequence 1, Appli
c	34	166.6	16.4	1203	3	US-09-544-618-6	Sequence 6, Appli
c	35	162.4	16.0	366	3	US-09-030-607-215	Sequence 215, App
c	36	162.4	16.0	366	3	US-09-439-313-215	Sequence 215, App
c	37	162.4	16.0	366	3	US-09-352-616A-215	Sequence 215, App
c	38	162.4	16.0	366	3	US-09-232-149A-215	Sequence 215, App
c	39	162.4	16.0	366	3	US-09-159-812-215	Sequence 215, App
c	40	162.4	16.0	366	3	US-09-636-215-215	Sequence 215, App
c	41	162.4	16.0	366	3	US-09-685-166A-215	Sequence 215, App
c	42	162.4	16.0	366	3	US-09-115-453-215	Sequence 215, App
c	43	162.4	16.0	366	3	US-09-688-489-215	Sequence 215, App
c	44	162.4	16.0	366	3	US-09-679-426-215	Sequence 215, App
c	45	162.4	16.0	366	3	US-09-759-143-215	Sequence 215, App

ALIGNMENTS

RESULT 1
US-09-455-486-1
; Sequence 1, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-I1
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1193
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (64)...(1083)
US-09-455-486-1

Query Match 100.0%; Score 1017; DB 3; Length 1193;
Best Local Similarity 100.0%; Pred. No. 2.5e-304;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303
```

```
Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

```
RESULT 2
US-09-323-873A-1
; Sequence 1, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
;  APPLICANT: Daniel E. Afar
;  APPLICANT:  Rene S. Hubert
;  APPLICANT:  Kahan Leong
;  APPLICANT:  Arthur B. Raitano
;  APPLICANT:  Douglas C. Saffran
;  APPLICANT:  Steve Chappell Mitchell
;  TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
;  TITLE OF INVENTION:  EXPRESSED IN HUMAN CANCERS AND USES THEREOF
;  FILE REFERENCE: 129.16USU2
;  CURRENT APPLICATION NUMBER: US/09/323,873A
;  CURRENT FILING DATE:  1999-06-01
;  PRIOR APPLICATION NUMBER: 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-09-323-873A-1

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-304;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965
```

```
Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 3
US-09-685-166A-878
; Sequence 878, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-685-166A-878

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-304;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 4
US-09-679-426-878
; Sequence 878, Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C20
;  CURRENT APPLICATION NUMBER: US/09/679,426
;  CURRENT FILING DATE:  2000-10-02
;  NUMBER OF SEQ ID NOS:  895
;  SOFTWARE:  FastSEQ for Windows Version 3.0
```

```
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-679-426-878

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-304;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 5
US-09-759-143-878
; Sequence 878, Application US/09759143
; Patent No. 6800746
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.427C23
;  CURRENT APPLICATION NUMBER: US/09/759,143
;  CURRENT FILING DATE:  2001-01-12
;  NUMBER OF SEQ ID NOS:  934
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-759-143-878

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-304;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485
```

```
Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 6
US-10-010-667A-1
; Sequence 1, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-010-667A-1

Query Match 100.0%; Score 1017; DB 3; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.5e-304;

Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 7
US-10-012-896-878

```
; Sequence 878, Application US/10012896
; Patent No. 6943236
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqiu
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel X.
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William T.
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Hural, John
;  APPLICANT:  McNeill, Patricia D.
;  APPLICANT:  Houghton, Raymond L.
;  APPLICANT:  Vinals de Bassols, Carlota
;  APPLICANT:  Foy, Teresa
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Wantanabe, Yoshihiro
;  APPLICANT:  Meagher, Madeleine Joy
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C27
;  CURRENT APPLICATION NUMBER: US/10/012,896
;  CURRENT FILING DATE:  2001-12-10
;  NUMBER OF SEQ ID NOS: 1011
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 878
;   LENGTH: 1195
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-012-896-878

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-304;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 8
US-09-949-016-2686
; Sequence 2686, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2686
;   LENGTH: 1147
;   TYPE: DNA
;   ORGANISM: Human
US-09-949-016-2686

  Query Match             99.8%;  Score 1015.4;  DB 3;  Length 1147;
  Best Local Similarity   99.9%;  Pred. No. 7.8e-304;
  Matches 1016;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         33 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 92
```

```
Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 152

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        153 CCTGTGCTTTTGCATTTGCAGCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 212

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 272

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 332

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 392

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 452

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 512

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 572

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 632

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 692

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 752

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 812

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 872

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 932

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 992

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1049
```

RESULT 9
US-09-323-873A-6
; Sequence 6, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2
; CURRENT APPLICATION NUMBER: US/09/323,873A
; CURRENT FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-323-873A-6

Query Match 74.8%; Score 760.6; DB 3; Length 3627;
Best Local Similarity 99.5%; Pred. No. 1.2e-224;
Matches 763; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 395

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 455

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 515

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 575

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 695

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 755

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 815

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAA 767
```

```
                ||||||||||||||||||||||||||||||||||||||||||   ||
Db        816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGTAAA 862
```

RESULT 10
US-09-455-486-4
; Sequence 4, Application US/09455486
; Patent No. 6833438
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Stephen C. Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.17-US-I1
; CURRENT APPLICATION NUMBER: US/09/455,486
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-455-486-4

```
  Query Match             74.8%;  Score 760.6;  DB 3;  Length 3627;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-224;
  Matches  763;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 395

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 455

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 515

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 575

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 695

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 755

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 815

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAA 767
              ||||||||||||||||||||||||||||||||||||||||||   ||
Db        816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGTAAA 862
```

RESULT 11
US-10-010-667A-6
; Sequence 6, Application US/10010667A
; Patent No. 6887975
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Hubert, Rene S.
; APPLICANT: Leong, Kahan
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Saffran, Douglas C.
; APPLICANT: Mitchell, Steve Chappell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 511582001601
; CURRENT APPLICATION NUMBER: US/10/010,667A
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 09/323,873
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: 60/087,520
; PRIOR FILING DATE: 1998-06-01
; PRIOR APPLICATION NUMBER: 60/091,183
; PRIOR FILING DATE: 1998-06-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 3627
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-010-667A-6

```
  Query Match             74.8%;  Score 760.6;  DB 3;  Length 3627;
  Best Local Similarity   99.5%;  Pred. No. 1.2e-224;
  Matches  763;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 155

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 215

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 275

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 335

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        336 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCCTTAGCAACT 395

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 455

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        456 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 515

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 575

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 635

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 695

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 755

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 815

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAA 767
              ||||||||||||||||||||||||||||||||||||||||||||    ||
Db        816 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGGTAAA 862
```

RESULT 12
US-09-439-313-342/c
; Sequence 342, Application US/09439313
; Patent No. 6329505
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang Yuqui
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael
; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; CURRENT FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 575
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-342

Query Match 50.7%; Score 516; DB 3; Length 592;
Best Local Similarity 99.6%; Pred. No. 2.4e-149;
Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 99

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 518
              |||||||: |||||||||||||||||||||||||||||
Db         38 AGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1
```

RESULT 13
US-09-352-616A-342/c
; Sequence 342, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqui
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
; LENGTH: 592
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-342

Query Match 50.7%; Score 516; DB 3; Length 592;
Best Local Similarity 99.6%; Pred. No. 2.4e-149;
Matches 516; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 99

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 518
              ||||||||: ||||||||||||||||||||||||||||
Db         38 AGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1


RESULT 14
US-09-636-215-342/c
; Sequence 342, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE:  210121.42717C17
;  CURRENT APPLICATION NUMBER: US/09/636,215
;  CURRENT FILING DATE:  2000-08-10
;  NUMBER OF SEQ ID NOS:  852
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-636-215-342

  Query Match             50.7%;  Score 516;  DB 3;  Length 592;
  Best Local Similarity   99.6%;  Pred. No. 2.4e-149;
  Matches  516;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 99

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 518
              ||||||||: ||||||||||||||||||||||||||||
Db         38 AGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1


RESULT 15
US-09-685-166A-342/c
; Sequence 342, Application US/09685166A
; Patent No. 6630305
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C21
;  CURRENT APPLICATION NUMBER: US/09/685,166A
;  CURRENT FILING DATE:  2000-10-10
;  NUMBER OF SEQ ID NOS: 898
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 342
;   LENGTH: 592
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-685-166A-342

  Query Match             50.7%;  Score 516;  DB 3;  Length 592;
  Best Local Similarity   99.6%;  Pred. No. 2.4e-149;
  Matches  516;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 459

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 399

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 339

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 279
```

```
Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 219

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 159

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 99

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 39

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGT 518
              ||||||||: |||||||||||||||||||||||||||
Db         38 AGAAAGCARATTGGGCTTCTCAGTTTCTTTTTTGCTGT 1
```

Search completed: December 5, 2005, 03:19:40
Job time : 205.756 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:13:31 ; Search time 682.751 Seconds
(without alignments)
9927.475 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaaagcagaaaagacat.....ctgagatatgttcccagttg 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1017	100.0	1177	14	ADV73174	Adv73174 Human col
2	1017	100.0	1193	3	AAZ49395	Aaz49395 Human STR
3	1017	100.0	1193	5	AAD07067	Aad07067 Human six
4	1017	100.0	1193	8	ACD02597	Acd02597 cDNA enco
5	1017	100.0	1193	14	ADY92698	Ady92698 Human STE
6	1017	100.0	1195	4	AAH93924	Aah93924 P789P ful
7	1017	100.0	1195	4	AAS64160	Aas64160 Human pro
8	1017	100.0	1195	5	ACA59968	Aca59968 Prostate
9	1017	100.0	1195	6	ABL95531	Abl95531 Human P78
10	1017	100.0	1195	6	ABK92128	Abk92128 Prostate
11	1017	100.0	1195	8	ACC95695	Acc95695 Prostate
12	1017	100.0	1195	10	ADB75572	Adb75572 Prostate
13	1017	100.0	1195	10	ADB14328	Adb14328 Human pro
14	1017	100.0	1195	10	AAD63162	Aad63162 Human STE
15	1017	100.0	1195	10	AAD62763	Aad62763 Human STE
16	1017	100.0	1195	10	ADG26744	Adg26744 Human pro
17	1017	100.0	1195	11	ADN39812	Adn39812 Cancer/an
18	1017	100.0	1195	11	ADN39395	Adn39395 Cancer/an
19	1017	100.0	1195	11	ADP88258	Adp88258 Prostate
20	1017	100.0	1195	12	ADL06462	Adl06462 Human tum
21	1017	100.0	1195	12	ADL06436	Adl06436 Human tum
22	1017	100.0	1195	12	ADJ75176	Adj75176 Marker ge
23	1017	100.0	1201	13	ADX33625	Adx33625 Plant ful
24	1017	100.0	1277	5	ADL46020	Adl46020 Human ova
25	1017	100.0	1294	4	AAK51978	Aak51978 Human pol
26	1017	100.0	1330	13	ADR14190	Adr14190 Human NP-
27	1017	100.0	1330	13	ADU06030	Adu06030 Novel bro
28	1017	100.0	1330	14	ADY15575	Ady15575 DNA encod
29	1017	100.0	1330	14	ADY19959	Ady19959 DNA encod
30	1004.4	98.8	1229	4	AAK52962	Aak52962 Human pol
31	1004	98.7	1198	8	ACD02628	Acd02628 STEAP-1 v
32	1002.4	98.6	1198	8	ACD02629	Acd02629 STEAP-1 v
33	988	97.1	1354	12	ADQ22300	Adq22300 Human sof
34	870	85.5	1365	8	ACD02599	Acd02599 cDNA enco
35	870	85.5	1365	8	ACD02630	Acd02630 STEAP-1 v
36	866	85.2	1369	8	ACD02632	Acd02632 STEAP-1 v
37	864.4	85.0	1369	8	ACD02631	Acd02631 STEAP-1 v
38	762.2	74.9	3627	8	ACD02601	Acd02601 cDNA enco
39	760.6	74.8	3627	3	AAZ49396	Aaz49396 Human STR
40	760.6	74.8	3627	5	AAD07071	Aad07071 Human six
41	760.6	74.8	3627	8	ACD02613	Acd02613 cDNA enco
42	760.6	74.8	3627	8	ACD02605	Acd02605 cDNA enco
43	760.6	74.8	3627	8	ACD02606	Acd02606 cDNA enco
44	760.6	74.8	3627	8	ACD02598	Acd02598 cDNA enco
45	760.6	74.8	3627	8	ACD02612	Acd02612 cDNA enco

ALIGNMENTS

RESULT 1
ADV73174
ID ADV73174 standard; DNA; 1177 BP.
XX
AC ADV73174;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human colon tumor cell upregulated gene SEQ ID NO 15.
XX
KW ds; gene; cancer; neoplasm; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004110345-A2.
XX
PD 23-DEC-2004.
XX
PF 28-OCT-2003; 2003WO-US034019.
XX
PR 29-OCT-2002; 2002US-0422176P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Bourner MJ, Bu JJ, Head RD, Hippenmeyer PJ, Klein BK;
PI Mazzarella RA, Staten NR;
XX
DR WPI; 2005-039958/04.
DR P-PSDB; ADV73212.
XX
PT New antibody that immunospecifically binds to p-cadherin, useful in
PT preparing a composition for treating or preventing a cancer-associated
PT disorder.
XX
PS Disclosure; SEQ ID NO 15; 257pp; English.
XX
CC The invention relates to an antibody immunospecifically binds to p-
CC cadherin or its fragment. The antibody is useful in preparing a
CC composition for treating or preventing a cancer-associated disorder. The
CC present sequence represents a gene upregulated in human colon cancer
CC cells.
XX

```
SQ   Sequence 1177 BP; 364 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1017;  DB 14;  Length 1177;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

```
RESULT 2
AAZ49395
ID   AAZ49395 standard; cDNA; 1193 BP.
XX
AC   AAZ49395;
XX
DT   14-MAR-2000  (first entry)
XX
DE   Human STRAP-1 cDNA.
XX
KW   Serpentine transmembrane antigen of the prostate; STRAP-1; prostate;
KW   transmembrane domain; type IIIa membrane protein; expression; cancer;
KW   prostate cancer; bladder cancer; colon cancer; pancreatic cancer;
KW   ovarian cancer; tumour antigen; immunisation; immune response; cellular;
KW   humoral; anticancer vaccine; antibody; detection; diagnosis; prognosis;
KW   monitoring; susceptibility; therapeutic inhibitor; drug targetting;
KW   recombinant protein; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .1083
FT                   /*tag=  a
FT                   /product= "Human STRAP-1 (serpentine transmembrane
FT                   antigen of the prostate)"
XX
PN   WO9962941-A2.
XX
PD   09-DEC-1999.
XX
PF   01-JUN-1999;   99WO-US012157.
XX
PR   01-JUN-1998;   98US-0087520P.
PR   30-JUN-1998;   98US-0091183P.
XX
PA   (UROG-) UROGENESYS INC.
PA   (AFAR/) AFAR D E.
PA   (HUBE/) HUBERT R S.
PA   (LEON/) LEONG K.
PA   (RAIT/) RAITANO A B.
PA   (SAFF/) SAFFRAN D C.
XX
PI   Afar DE,  Hubert RS,  Leong K,  Raitano AB,  Saffran DC;
XX
DR   WPI; 2000-072832/06.
DR   P-PSDB; AAY58194.
XX
PT   Novel proteins useful as diagnostic markers and therapeutic targets,
PT   particularly for prostatic cancer.
XX
PS   Claim 4; Fig 1A; 83pp; English.
XX
CC   This sequence represents cDNA encoding a novel human protein, STRAP-1
CC   (serpentine transmembrane antigen of the prostate). STRAP-1 is the
CC   prototype member of the STRAP family of proteins (AAY58194-Y58197) which
CC   exhibit a high degree of structural conservation, but which show no
CC   significant structural homology to known human proteins. The STRAP-1 gene
CC   has been localised to chromosome 7p22. STRAP-1 is thought to be a type
CC   IIIa membrane protein and is expressed predominantly in prostate cells in
CC   normal human tissues. Structurally, STRAP-1 is a 339 amino acid protein
CC   characterised by six transmembrane domains and intracellular N- and C-
CC   termini, suggesting that it folds in a "serpentine" manner into three
CC   extracellular and two intracellular loops. STRAP-1 mRNA and protein
CC   expression is maintained at high levels and throughout all stages of
CC   prostate cancer. STRAP-1 mRNA and/or protein is also overexpressed in
CC   certain other cancers, including bladder, colon, pancreatic and ovarian
CC   cancer. The function of the STRAP proteins is not known. They may be ion
CC   channels (from the presence of six transmembrane domains, a feature which
CC   is shared by certain ion channels) or gap-junction proteins (from
CC   immunohistochemical staining). STRAP-1 and STRAP-2 are cell-surface
CC   tumour antigens. Immunisation with a STRAP protein induces cellular and
```

```
CC   humoral immune responses against STRAP-expressing cells. STRAP proteins
CC   may be used to identify specific-binding agents, to produce anticancer
CC   vaccines and to generate specific antibodies. The antibodies may be used
CC   for detection, prognosis, and monitoring of cancers (or susceptibility to
CC   cancer), as therapeutic inhibitors or to target therapeutic agents to
CC   their site of action. STRAP nucleic acids may be used for recombinant
CC   protein production, as diagnostic and prognostic reagents, for
CC   identifying STRAP-expressing cells for screening inhibitors of STRAP
CC   expression and for therapeutic modulation/inhibition of STRAP expression.
CC   Since high levels of STRAP proteins are exposed on the cell surface, they
CC   are easily targetted by systemically administered agents, and because
CC   they are expressed mainly on prostatic epithelial cells, agents targetted
CC   to them should have minimal side effects on other tissues
XX
SQ   Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1017;  DB 3;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 3
AAD07067
ID   AAD07067 standard; cDNA; 1193 BP.
XX
AC   AAD07067;
XX
DT   06-AUG-2001  (first entry)
XX
DE   Human six transmembrane epithelial antigen of prostate-1 clone 10 cDNA.
XX
KW   Human; cytostatic; antiproliferative; vaccine; gene therapy;
KW   six transmembrane epithelial antigen of the prostate-1; STEAP-1;
KW   chromosome 7p22.3; cancer; prostate; colon; bladder; lung; ovarian;
KW   pancreatic; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             64. .1191
FT                   /*tag= a
FT                   /product= "Human six transmembrane epithelial antigen of
FT                   the prostate (STEAP)-1"
FT                   /note= "CDS does not include stop codon"
FT                   /transl_except= (pos:1078. .1086, aa:Leu-Asn)
FT                   /note= "Inframe stop codon alters the reading frame"
FT                   /partial
XX
PN   WO200140276-A2.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033040.
XX
PR   06-DEC-1999;   99US-00455486.
XX
PA   (UROG-) UROGENESYS INC.
XX
PI   Afar DEH,  Hubert RS,  Raitano AB,  Saffran DC,  Mitchell SC;
PI   Faris M,  Jakobovits A;
XX
DR   WPI; 2001-367804/38.
DR   P-PSDB; AAE02780.
XX
PT   New STEAP (six transmembrane epithelial antigen of the prostate)
PT   proteins, expressed in human cancers, useful for detecting and treating
PT   cancer.
XX
PS   Example 2; Fig 1A-1B; 187pp; English.
XX
CC   The present sequence is human six transmembrane epithelial antigen of the
CC   prostate (STEAP)-1 clone 10 cDNA. STEAP is a member of cell surface
CC   serpentine transmembrane antigens. STEAP-1 gene is located on chromosome
CC   7p22.3 and is used in gene therapy. Inhibiting the development or
CC   progression of a cancer (eg. prostate, colon, bladder, lung, ovarian and
CC   pancreatic) expressing STEAP or inhibiting growth or killing cells
CC   expressing STEAP in a patient, comprises administering a vaccine
CC   composition to the patient. Treating a patient with a cancer that
```

```
CC   expresses STEAP, or inhibiting growth or killing cells expressing STEAP,
CC   comprises administering to the patient a vector encoding single chain
CC   monoclonal antibody that comprises the variable domains of the heavy and
CC   light chains of the monoclonal antibody that specifically binds to STEAP,
CC   such that the vector delivers the single chain monoclonal antibody coding
CC   sequence to the cancer cells and the encoded single chain monoclonal
CC   antibody is expressed intracellularly. Note: The present sequence is also
CC   shown in sequence listing of the specification, but it lacks nulceotides
CC   at its 5' end
XX
SQ   Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1017;  DB 5;  Length 1193;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 4
ACD02597
ID   ACD02597 standard; cDNA; 1193 BP.
XX
AC   ACD02597;
XX
DT   31-JUL-2003  (first entry)
XX
DE   cDNA encoding novel human gene STEAP-1 variant 1.
XX
KW   STEAP-1; six transmembrane epithelial antigen of the prostate; cancer;
KW   cancer vaccine; delineation; cytogenetic abnormality; cytostatic;
KW   vaccine; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003022995-A2.
XX
PD   20-MAR-2003.
XX
PF   06-SEP-2002; 2002WO-US028371.
XX
PR   06-SEP-2001; 2001US-0317840P.
PR   05-APR-2002; 2002US-0370387P.
XX
PA   (AGEN-) AGENSYS INC.
XX
PI   Faris M,  Ge W,  Raitano AB,  Challita-Eid PM,  Jakobovits A;
XX
DR   WPI; 2003-313240/30.
DR   P-PSDB; ABU98383.
XX
PT   New composition comprising a substance that modulates the status of a
PT   STEAP-1-related protein, useful for treating and detecting cancer.
XX
PS   Example 2; Fig 2A; 248pp; English.
XX
CC   The invention describes a composition comprising a substance that
CC   modulates the status of a protein (I) of 340 or 283 amino acids, or of
CC   any of the 15 sequences of 259 amino acids, given in the specification,
CC   or a molecule that is modulated by the protein, where the status of the
CC   cell that expresses the protein is modulated. The compositions, proteins,
CC   polynucleotides and methods are useful for treating and detecting cancer.
CC   The STEAP-1-related proteins are useful for generating cancer vaccines.
CC   The polynucleotides are useful as tools for delineating, with greater
CC   precision, cytogenetic abnormalities in the chromosomal region that
CC   encodes STEAP-1 that may contribute to the malignant phenotype. This
CC   sequence encodes a variant of human six transmembrane epithelial antigen
CC   of the prostate or STEAP-1
XX
SQ   Sequence 1193 BP; 382 A; 221 C; 233 G; 357 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1017;  DB 8;  Length 1193;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

```
RESULT 5
ADY92698
ID   ADY92698 standard; cDNA; 1193 BP.
XX
AC   ADY92698;
XX
DT   02-JUN-2005  (first entry)
XX
DE   Human STEAP-1 (8P1B4) clone 10 cDNA, SEQ ID NO: 1.
XX
KW   Vaccine; antibody therapy; immune stimulation; gene amplification;
KW   prostate tumor; cytostatic; andrology; genitourinary disease; neoplasm;
KW   cancer; six transmembrane epithelial antigen of prostate 1; STEAP-1;
KW   chromosome 7; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             64..1191
FT                   /*tag= b
FT                   /product= "Human STEAP-1 protein #2"
FT                   /transl_except= (pos:1078..1086, aa:Leu-Asn)
FT                   /partial
FT                   /note= "No stop codon"
FT   CDS             64..1083
FT                   /*tag= a
FT                   /product= "Human STEAP-1 protein #1"
XX
PN   US2005063975-A1.
XX
PD   24-MAR-2005.
XX
PF   05-JAN-2004; 2004US-00752421.
XX
PR   01-JUN-1999;   99US-00323873.
PR   06-DEC-1999;   99US-00455486.
XX
PA   (AFAR/) AFAR D E H.
PA   (HUBE/) HUBERT R S.
PA   (RAIT/) RAITANO A B.
PA   (SAFF/) SAFFRAN D.
PA   (MITC/) MITCHELL S C.
XX
PI   Afar DEH,  Hubert RS,  Raitano AB,  Saffran D,  Mitchell SC;
XX
DR   WPI; 2005-252610/26.
DR   P-PSDB; ADY92699, ADY92744.
XX
PT   Novel isolated polynucleotide that encodes six transmembrane epithelial
PT   antigen of prostate polypeptide, useful for diagnosing or treating
PT   prostate cancer.
XX
PS   Example 1; SEQ ID NO 1; 80pp; English.
XX
CC   The invention relates to cell surface serpentine transmembrane antigens
CC   predominantly expressed in the prostate termed as six transmembrane
CC   epithelial antigen of prostate (STEAP-2) and their corresponding nucleic
CC   acid sequences. STEAP-2 DNA is useful for diagnosing or treating prostate
CC   cancer. It can be used as a primer or probe for the amplification and/or
CC   detection of STEAP genes and as a tool for modulating or inhibiting the
CC   expression of the STEAP genes. STEAP-2 DNA is also useful in cancer
CC   vaccines for the generation of therapeutic or prophylactic immunity
CC   against prostate cancer. STEAP antibodies are useful in antibody therapy.
CC   The present sequence is the human STEAP-1 cDNA. Human STEAP-1 gene maps
CC   within chromosome 7p22 (7p2.3).
XX
SQ   Sequence 1193 BP; 382 A; 219 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1017;  DB 14;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080
```

RESULT 6
AAH93924
ID AAH93924 standard; cDNA; 1195 BP.
XX
AC AAH93924;
XX
DT 04-OCT-2001 (first entry)
XX
DE P789P full length cDNA sequence.
XX
KW Human; prostate cancer; prostate-specific; diagnosis; vaccine;
KW cytostatic; gene therapy; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200151633-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001574.
XX
PR 14-JAN-2000; 2000US-00483672.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG;
PI Kalos MD, Panger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW;
PI Wang A, Meagher MJ;
XX
DR WPI; 2001-425873/45.
XX
PT New polynucleotide encoding a prostate-specific protein, for diagnosing,
PT monitoring and treating prostate cancer in a patient and for use in
PT vaccines.
XX
PS Claim 1; Page 510; 543pp; English.
XX
CC The present invention describes polynucleotide sequences (I) which encode
CC prostate-specific proteins (II). (I) and (II) have cytostatic activity,
CC and can be used in vaccine production and gene therapy. (I), (II),
CC antibodies to (II), fusion proteins comprising (II), and isolated T cells
CC prepared using (I) or (II) are used treat cancer in a patient. (I) and
CC the antibodies are also used in the detection of cancer in a patient. The
CC cancer that is diagnosed or treated is particularly prostate cancer. (I)
CC and (II) can be used in vaccines. The antibodies or (I) can be used for
CC monitoring the progression of cancer in a patient. (I) and (II) can also
CC be used to improve diagnostic and therapeutic methods for prostate
CC cancer. They can indicate the level of metastasis as well as the prostate
CC volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent
CC polynucleotide and amino acid sequences used in the exemplification of
CC the present invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 4; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
```

```
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 7
AAS64160
ID AAS64160 standard; cDNA; 1195 BP.
XX
AC AAS64160;
XX
DT 29-JAN-2002 (first entry)
XX
DE Human prostate cDNA sequence #590.
XX
KW Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
XX
OS Homo sapiens.
XX
PN WO200173032-A2.
XX
PD 04-OCT-2001.
XX
PF 27-MAR-2001; 2001WO-US009919.
XX
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2001-639232/73.
DR P-PSDB; AAU69927.
XX
PT New human prostate-specific polypeptides and polynucleotides useful for
PT the diagnosis and treatment of cancer, especially prostate cancer.
XX
PS Claim 1; Page 548; 579pp; English.
XX
CC The invention relates to isolated prostate-specific polynucleotides,
CC polypeptides, fusion proteins of the polypeptides, antibodies raised
CC against the polypeptides (or antigenic epitopes derived from them) and
CC antigen-presenting cells expressing the polypeptides. The antibodies are
CC useful for detecting the presence of cancer, especially prostate cancer.
CC The polypeptides, polynucleotides and the antigen-presenting cells are
CC useful for stimulating and/or expanding T cells specific for a tumour
CC protein, and for inhibiting the development of cancer especially prostate
CC cancer. Compositions comprising the polynucleotide and/or polypeptide are
CC useful for stimulating an immune response, and for treating cancer. The
CC oligonucleotide is useful for detecting cancer. The present sequence is a
CC prostate specific polynucleotide of the invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

```
  Query Match             100.0%;  Score 1017;  DB 4;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 8
ACA59968
ID ACA59968 standard; cDNA; 1195 BP.
XX
AC ACA59968;
XX
DT 10-JUN-2003 (first entry)
XX
DE Prostate cancer therapy associated cDNA #655.
XX
KW Prostate cancer; vaccine; gene therapy; cytostatic; fusion protein;
KW immunogen; cancer; prostate specific antigen; PSA;
KW prostatic acid phosphatase; PAP; prostate specific membrane antigen;
KW PSMA; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002192763-A1.
XX
PD 19-DEC-2002.
XX
PF 29-JUN-2001; 2001US-00895793.
XX
PR 04-OCT-1999; 99US-0157455P.
PR 04-OCT-2000; 2000US-00679272.
PR 28-MAR-2001; 2001US-00822827.
XX
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
PA (HURA/) HURAL J.
PA (MCNE/) MCNEILL P D.
PA (HOUG/) HOUGHTON R L.
PA (DBAS/) Y DE BASSOLS C V.
PA (FOYT/) FOY T M.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA, Hural J;
PI Mcneill PD, Houghton RL, Y De BassolsCV, Foy TM;
XX
DR WPI; 2001-245062/25.
DR P-PSDB; ABU71821.
XX
PT Prostate specific protein and its encoding polynucleotide, useful for the
PT treatment and diagnosis of prostate cancer.
XX
PS Example 5; SEQ ID NO 878; 85pp; English.
XX
CC The invention describes a fusion protein comprising at least one amino
CC acid sequence of immunogenic portions of any of the 3 sequences not
CC defined in the specification, or sequences having at least 70 or 90 %
CC sequence identity to any one of the 35 sequences defined in the USPTO web
CC site, which is encoded by any of the 4 nucleotide sequences not defined
CC in the specification. The fusion protein, composition and methods are
CC useful for diagnosing, preventing and/or treating cancer, particularly
CC prostate cancer. The proteins are useful as markers to indicate the
CC presence or absence of cancer. This sequence represents a prostate cancer
CC therapy associated cDNA. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20020192763
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 1017;  DB 5;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605
```

```
Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 9
ABL95531
ID ABL95531 standard; cDNA; 1195 BP.
XX
AC ABL95531;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human P789P cDNA sequence SEQ ID NO 878.
XX
KW Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
KW gene therapy; gene; ss.
XX
OS Homo sapiens.
XX
PN US2002022248-A1.
XX
PD 21-FEB-2002.
XX
PF 12-JAN-2001; 2001US-00759143.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 10-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 10-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
XX
PA (XUJJ/) XU J.
PA (DILL/) DILLON D C.
PA (MITC/) MITCHAM J L.
PA (HARL/) HARLOCKER S L.
PA (JIAN/) JIANG Y.
PA (KALO/) KALOS M D.
PA (FANG/) FANGER G R.
PA (RETT/) RETTER M W.
PA (STOL/) STOLK J A.
PA (DAYC/) DAY C H.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (LISX/) LI S X.
PA (WANG/) WANG A.
PA (SKEI/) SKEIKY Y A W.
PA (HEPL/) HEPLER W T.
PA (HEND/) HENDERSON R A.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Kalos MD;
PI Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Carter D;
PI Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
XX
DR WPI; 2002-255649/30.
XX
PT New prostate-specific polynucleotides for diagnosing and treating
PT diseases, in particular prostate cancer, and as markers for the
PT progression of cancer.
XX
PS Claim 1; SEQ ID NO 878; 87pp; English.
XX
CC The present invention provides prostate-specific coding sequences and
CC their encoded proteins. These can be used in the diagnosis and treatment
CC of cancers, particularly prostate cancer. The present sequence is a cDNA
CC described in the invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485
```

```
Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 10
ABK92128
ID ABK92128 standard; DNA; 1195 BP.
XX
AC ABK92128;
XX
DT 15-AUG-2002 (first entry)
XX
DE Prostate cancer-associated DNA sequence #14.
XX
KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.
XX
OS Mammalia.
XX
PN WO200230268-A2.
XX
PD 18-APR-2002.
XX
PF 12-OCT-2001; 2001WO-US032045.
XX
PR 13-OCT-2000; 2000US-00687576.
PR 08-DEC-2000; 2000US-00733288.
PR 08-DEC-2000; 2000US-00733742.
PR 24-JAN-2001; 2001US-0263957P.
PR 16-MAR-2001; 2001US-0276791P.
PR 16-MAR-2001; 2001US-0276888P.
PR 06-APR-2001; 2001US-0281922P.
PR 24-APR-2001; 2001US-0286214P.
PR 30-APR-2001; 2001US-00847046.
PR 04-MAY-2001; 2001US-0288589P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX
DR WPI; 2002-471335/50.
DR P-PSDB; ABG61813.
XX
PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.
XX
PS Claim 22; Page 311-312; 436pp; English.
XX
CC The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridise to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605
```

```
Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 11
ACC95695
ID ACC95695 standard; cDNA; 1195 BP.
XX
AC ACC95695;
XX
DT 28-AUG-2003 (first entry)
XX
DE Prostate tumour specific cDNA sequence SEQ ID 878.
XX
KW Cytostatic; gene therapy; prostate-specific protein; PSP; human;
KW immune response; prostate cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200289747-A2.
XX
PD 14-NOV-2002.
XX
PF 09-MAY-2002; 2002WO-US014753.
XX
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Henderson RA;
PI Kalos MD, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS;
PI Carter D, Li SX, Wang A, Skeiky YAW, Hepler WT, Hural J;
PI Mcneill PD, Houghton RL, Vinals Y De BassolsC, Foy TM, Watanabe Y;
PI Deng T;
XX
DR WPI; 2003-167130/16.
XX
PT New prostate-specific proteins and genes, useful in gene therapy,
PT particularly for stimulating an immune response in a patient, or treating
PT prostate cancer in a patient, as well as for diagnosing prostate cancer
PT in a patient.
XX
PS Example 5; Page 617-618; 691pp; English.
XX
CC The present invention relates to novel prostate-specific proteins (PSP)
CC and their coding sequences. The PSPs and their coding sequences are
CC useful for stimulating an immune response in a patient, or for treating
CC prostate cancer in a patient and for determining, detecting or diagnosing
CC the presence of a cancer in a patient. The present sequence was used to
CC illustrate the invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 8; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 12
ADB75572
ID   ADB75572 standard; cDNA; 1195 BP.
XX
AC   ADB75572;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Prostate cancer marker cDNA.
XX
KW   Prostate; cancer; cytostatic; gene therapy; marker; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003009814-A2.
XX
PD   06-FEB-2003.
XX
PF   25-JUL-2002; 2002WO-US023913.
XX
PR   25-JUL-2001; 2001US-0307982P.
PR   22-AUG-2001; 2001US-0314356P.
PR   25-SEP-2001; 2001US-0325020P.
PR   12-DEC-2001; 2001US-0341746P.
PR   05-MAR-2002; 2002US-0362158P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbatcheva B;
PI   Hoersh S, Kamatkar S, Wonsey AM, Glatt K, Zhao X, Anderson D;
XX
DR   WPI; 2003-248033/24.
XX
PT   New nucleic acid molecule, useful for diagnosing or treating prostate
PT   cancer.
XX
PS   Disclosure; SEQ ID NO 396; 99pp; English.
XX
CC   The invention relates to newly discovered cancer markers associated with
CC   the cancerous state of prostate cells. Also disclosed is a method of
CC   assessing whether a patient is afflicted with prostate cancer. The method
CC   of the invention involves assessing whether a patient is afflicted with
CC   prostate cancer by comparing the level of expression of a marker in a
CC   patient sample and the normal level of expression of the marker in a
CC   control non-prostate cancer sample, where a significant increase in the
CC   level of expression of the marker in the patient sample and the normal
CC   level indicates that the patient is afflicted with prostate cancer.
CC   Nucleic acids of the invention are useful for diagnosing or treating
CC   prostate cancer, and may be useful in gene therapy. Sequences given in
CC   ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
CC   data for this patent did not form part of the printed specification, but
CC   was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1017;  DB 10;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-276;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 13
ADB14328
ID   ADB14328 standard; cDNA; 1195 BP.
XX
AC   ADB14328;
```

XX
DT 18-DEC-2003 (first entry)
XX
DE Human prostate specific full length cDNA P789P.
XX
KW Human; ss; prostate specific cDNA; cytostatic; immunostimulant;
KW gene therapy; cell therapy; vaccine; T-cell epitope;
KW class I major histocompatibility complex allele; MHC; prostate cancer;
KW tumour; antigen presenting cell.
XX
OS Homo sapiens.
XX
PN US2003185830-A1.
XX
PD 02-OCT-2003.
XX
PF 12-NOV-2002; 2002US-00294025.
XX
PR 25-FEB-1997; 97US-00806099.
PR 01-AUG-1997; 97US-00904804.
PR 09-FEB-1998; 98US-00020956.
PR 25-FEB-1998; 98US-00030607.
PR 14-JUL-1998; 98US-00115453.
PR 23-SEP-1998; 98US-00159812.
PR 15-JAN-1999; 99US-00232149.
PR 09-APR-1999; 99US-00288946.
PR 13-JUL-1999; 99US-00352616.
PR 12-NOV-1999; 99US-00439313.
PR 18-NOV-1999; 99US-00443686.
PR 14-JAN-2000; 2000US-00483672.
PR 27-MAR-2000; 2000US-00536857.
PR 09-MAY-2000; 2000US-00568100.
PR 12-MAY-2000; 2000US-00570737.
PR 13-JUN-2000; 2000US-00593793.
PR 27-JUN-2000; 2000US-00605783.
PR 09-AUG-2000; 2000US-00636215.
PR 29-AUG-2000; 2000US-00651236.
PR 06-SEP-2000; 2000US-00657279.
PR 02-OCT-2000; 2000US-00679426.
PR 10-OCT-2000; 2000US-00685166.
PR 09-NOV-2000; 2000US-00709729.
PR 12-JAN-2001; 2001US-00759143.
PR 09-FEB-2001; 2001US-00780669.
PR 09-MAY-2001; 2001US-00852911.
PR 29-JUN-2001; 2001US-00895814.
PR 10-DEC-2001; 2001US-00012896.
PR 09-MAY-2002; 2002US-00144678.
XX
PA (CORI-) CORIXA CORP.
XX
PI Xu J, Stolk JA, Kalos MD;
XX
DR WPI; 2003-756193/71.
DR P-PSDB; ADB14329.
XX
PT New isolated polypeptide for use in a vaccine for stimulating an immune
PT response, or for treating or diagnosis cancer, preferably prostate
PT cancer.
XX
PS Example 5; Page; 101pp; English.
XX
CC The invention relates to an isolated polypeptide comprising no more than
CC 11-542 amino acids of ADB13563 comprising a sequence ADB14487. The
CC peptides comprise a fragment ADB13563 of that contain naturally processed
CC T-cell epitopes for 3 class I major histocompatibility complex (MHC)
CC alleles. ADB13563 is a polypeptide encoded by a human prostate specific
CC cDNA, one of 648 disclosed as new. Also included are nucleic acids
CC encoding the proteins and peptides, expression vectors, a host cell
CC transformed with the vector, an isolated antibody (or antigen binding
CC fragment) that specifically binds to the protein or peptide, detecting
CC the presence of a cancer in a patient (comprising contacting a patient
CC sample with a binding agent that binds to the peptides or a polypeptide
CC appearing as ADB13558, detecting the amount of polypeptide that binds to
CC the agent and comparing the amount of polypeptide to a predetermined cut-
CC off value to determine the presence of cancer), a fusion protein
CC comprising the peptides or proteins, stimulating or expanding T cells
CC specific for a tumour protein comprising contacting T cells with the
CC peptides or the isolated T cell population, treating prostate cancer in a
CC patient comprising administering a composition comprising the peptides,
CC nucleic acids, antibodies or compounds, determining the presence of a
CC cancer in a patient and treating prostate cancer in a patient comprising
CC incubating cluster of differentiation (CD4+) and/or CD8+ T cells isolated
CC from a patient with the peptides or antigen presenting cells that express
CC (the peptides so that the T cells proliferate, and administering the
CC proliferated T cells to the patient. The peptides (or an oligonucleotide
CC that hybridises to nucleic acid encoding them), is used to detect the
CC presence of cancer in a patient. The peptides, nucleic acids encoding, or
CC antigen-presenting cells expressing the nucleic acid, are used to
CC stimulate or expand T cells specific for a tumour protein. The peptides,
CC nucleic acids, antibodies, fusion proteins, T cell populations or antigen
CC presenting cells are used to stimulate an immune response or treat
CC prostate cancer in a patient. The present sequence is a known cDNA
CC showing sequence similarity to one of the disclosed human prostate
CC specific cDNAs. Note: Except where otherwise indicated, the sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?DocID=20030185830.
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 10; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 14
AAD63162
ID AAD63162 standard; DNA; 1195 BP.
XX
AC AAD63162;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
KW Human; breast cancer; metastasis; differential modulation; therapy;
KW STEAP; six transmembrane epithelial antigen of the prostate; ds.
XX
OS Homo sapiens.
XX
PN US2003190656-A1.
XX
PD 09-OCT-2003.
XX
PF 21-MAR-2003; 2003US-00393590.
XX
PR 29-MAR-2002; 2002US-0368789P.
XX
PA (WANG/) WANG Y.
XX
PI Wang Y;
XX
DR WPI; 2003-831621/77.
XX
PT Prognosticating metastasis in a breast cancer patient comprises
PT identifying differential modulation of each gene relative to the
PT expression of the same genes in a normal population in combination of
PT genes.
XX
PS Example 2; Page 54-55; 0pp; English.
XX
CC The present invention relates to a method of prognosticating metastasis
CC in a breast cancer patient involves identifying differential modulation
CC of each gene relative to the expression of the same genes in a normal
CC population in combination of genes. The invention is useful for
CC prognosticating breast cancer in a patient. The present sequence is human
CC STEAP (six transmembrane epithelial antigen of the prostate) DNA used to
CC illustrate the method of the invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

```
Query Match           100.0%;  Score 1017;  DB 10;  Length 1195;
Best Local Similarity  100.0%;  Pred. No. 2.6e-276;
Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

RESULT 15
AAD62763
ID AAD62763 standard; DNA; 1195 BP.
XX
AC AAD62763;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human STEAP (six transmembrane epithelial antigen of the prostate) DNA.
XX
KW Human; cancer; differential modulation; gene expression profile; STEAP;
KW six transmembrane epithelial antigen of the prostate; ds.
XX
OS Homo sapiens.
XX
PN US2003194733-A1.
XX
PD 16-OCT-2003.
XX
PF 21-MAR-2003; 2003US-00393567.
XX
PR 29-MAR-2002; 2002US-0368667P.
XX
PA (WANG/) WANG Y.
XX
PI Wang Y;
XX
DR WPI; 2003-844450/78.
XX
PT Diagnosing cancer comprises identifying differential modulation of each
PT gene (relative to the expression of the same genes in a normal
PT population) in a combination of genes.
XX
PS Claim 4; Page 54-55; 0pp; English.
XX
CC The invention relates to a method for diagnosing cancer. The method
CC comprising identifying differential modulation of each gene (relative to
CC the expression of the same genes in a normal population) in a combination
CC of genes. The method, diagnostic portfolio and the kit are useful in
CC diagnosing cancer. The method may also be used for determining gene
CC expression profiles. The present sequence is human STEAP (six
CC transmembrane epithelial antigen of the prostate) DNA used to illustrate
CC the method of the invention
XX
SQ Sequence 1195 BP; 382 A; 221 C; 233 G; 359 T; 0 U; 0 Other;

Query Match 100.0%; Score 1017; DB 10; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-276;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

Search completed: December 4, 2005, 21:08:44
Job time : 685.751 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:37:01 ; Search time 5376.03 Seconds
(without alignments)
10753.247 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaaagcagaaaagacat.....ctgagatatgttcccagttg 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1017	100.0	1193	6	BD232184	BD232184 Novel ser
2	1017	100.0	1193	6	AR617054	AR617054 Sequence
3	1017	100.0	1193	6	AX155243	AX155243 Sequence
4	1017	100.0	1195	6	CQ776742	CQ776742 Sequence
5	1017	100.0	1195	6	AR366780	AR366780 Sequence
6	1017	100.0	1195	6	AR405830	AR405830 Sequence
7	1017	100.0	1195	6	AR564210	AR564210 Sequence
8	1017	100.0	1195	6	AR589196	AR589196 Sequence
9	1017	100.0	1195	6	AR654075	AR654075 Sequence
10	1017	100.0	1195	6	AX201105	AX201105 Sequence
11	1017	100.0	1195	6	AX267904	AX267904 Sequence
12	1017	100.0	1195	6	AX926483	AX926483 Sequence
13	1017	100.0	1195	6	AX951736	AX951736 Sequence
14	1017	100.0	1195	6	AX960014	AX960014 Sequence
15	1017	100.0	1195	8	AF186249	AF186249 Homo sapi
16	1017	100.0	1240	8	BC011802	BC011802 Homo sapi
17	1017	100.0	1277	6	CQ412839	CQ412839 Sequence
18	1017	100.0	1330	6	CQ981397	CQ981397 Sequence
19	1017	100.0	1330	6	CS031875	CS031875 Sequence
20	1017	100.0	1330	6	CS036259	CS036259 Sequence
21	1017	100.0	1330	6	CS040827	CS040827 Sequence
22	1017	100.0	1330	6	CS045211	CS045211 Sequence
23	844.2	83.0	1754	4	AF319659	AF319659 Sus scrof
24	760.6	74.8	3627	6	BD232188	BD232188 Novel ser
25	760.6	74.8	3627	6	AR366784	AR366784 Sequence
26	760.6	74.8	3627	6	AR617056	AR617056 Sequence
27	760.6	74.8	3627	6	AR654079	AR654079 Sequence
28	760.6	74.8	3627	6	AX155248	AX155248 Sequence
29	738.6	72.6	1234	9	BC061023	BC061023 Mus muscu
30	737	72.5	1175	9	AF297098	AF297098 Mus muscu
31	737	72.5	1211	6	CQ777614	CQ777614 Sequence
32	719.4	70.7	1198	6	BD192004	BD192004 Modulator
33	636.2	62.6	1191	9	AY029584	AY029584 Mus muscu
34	615.6	60.5	1209	8	BC066301	BC066301 Homo sapi
35	517.2	50.9	87401	14	AC021898	AC021898 Homo sapi
36	517.2	50.9	105247	8	AC004969	AC004969 Homo sapi
c 37	517.2	50.9	110000	14	AC147308_0	AC147308 Pan trogl
38	517.2	50.9	157646	8	AC142337	AC142337 Pan trogl
39	517.2	50.9	161732	14	AC104475	AC104475 Pan trogl
c 40	517.2	50.9	211383	8	AC161278	AC161278 Pan trogl
41	517.2	50.9	219769	14	AC162380	AC162380 Pan trogl
c 42	516	50.7	592	6	BD242240	BD242240 Compounds
c 43	516	50.7	592	6	AR278447	AR278447 Sequence
c 44	516	50.7	592	6	AR367143	AR367143 Sequence
c 45	516	50.7	592	6	AR371039	AR371039 Sequence

ALIGNMENTS

RESULT 1
BD232184
LOCUS BD232184 1193 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel serpiginous transmembrane antigen expressed in human cancer and utilization thereof.
ACCESSION BD232184
VERSION BD232184.1 GI:33041954
KEYWORDS JP 2002517184-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1193)
AUTHORS Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and Mitchell,S.C.
TITLE Novel serpiginous transmembrane antigen expressed in human cancer and utilization thereof
JOURNAL Patent: JP 2002517184-A 1 18-JUN-2002;
UROGENESYS INC
COMMENT OS Homo sapiens (human)
PN JP 2002517184-A/1
PD 18-JUN-2002
PF 01-JUN-1999 JP 2000552151
PR 01-JUN-1998 US 60/087520,30-JUN-1998 US 60/091183 PI DANIEL E AFAR,RENE S HUBERT,KAHAN LEONG,ARTHUR B RAITANO PI ,DOUGLAS C SAFFRAN,
PI STEPHEN CHAPPELL MITCHELL
PC C12N15/09,A61K38/00,A61K39/395,A61P35/00,C07K14/47,C07K16/18,
PC C12N5/10,
PC C12P21/00,C12P21/08,C12Q1/68,G01N33/574,C12N15/00,A61K37/02,
PC C12N5/00
CC Novel serpiginous transmembrane antigen expressed in human CC cancer and
CC utilization thereof
FH Key Location/Qualifiers
FT source 1. .1193
FT /organism='Homo sapiens (human)'.
FEATURES Location/Qualifiers
source 1. .1193
/organism="Homo sapiens"

```
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 2
AR617054
LOCUS       AR617054               1193 bp    DNA     linear   PAT 14-FEB-2005
DEFINITION  Sequence 1 from patent US 6833438.
ACCESSION   AR617054
VERSION     AR617054.1  GI:59720558
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1193)
  AUTHORS   Afar,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE     Serpentine transmembrane antigens expressed in human cancers and
            uses thereof
  JOURNAL   Patent: US 6833438-A 1 21-DEC-2004;
            Agensys, Inc.; Santa Monica, CA
FEATURES             Location/Qualifiers
     source          1. .1193
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1193;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 3
AX155243
LOCUS       AX155243               1193 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 1 from Patent WO0140276.
ACCESSION   AX155243
VERSION     AX155243.1  GI:14536707
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Afar,D.E., Hubert,R.S., Raitano,A.B., Saffran,D.C., Mitchell,S.C.,
            Faris,M. and Jakobovits,A.
  TITLE     Serpentine transmembrane antigens expressed in human prostate
            cancers and uses thereof
  JOURNAL   Patent: WO 0140276-A 1 07-JUN-2001;
            Urogenesys, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1193
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             64. .1083
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC42677.1"
                     /db_xref="GI:14536708"
                     /translation="MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLL
                     HLHQTAHADEFDCPSELQHTQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSH
                     QQYFYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLT
                     RKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                     YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
                     WIDIKQFVWYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTE
                     ICSQL"
ORIGIN

  Query Match           100.0%;  Score 1017;  DB 6;  Length 1193;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 123

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 183

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 243

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 303

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 363

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 423

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 483

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 543

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 603

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 663

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 723

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 783

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 843

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 903

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 963

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1023

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1024 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1080


RESULT 4
CQ776742
LOCUS       CQ776742               1195 bp    DNA     linear   PAT 11-MAR-2004
DEFINITION  Sequence 428 from Patent EP1394274.
ACCESSION   CQ776742
VERSION     CQ776742.1  GI:45380132
KEYWORDS    .
SOURCE      Homo sapiens (human)
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ohtani,N., Sugita,Y., Yamaya,M., Kubo,H., Nagai,H. and Izuhara,K.
  TITLE     Methods of testing for bronchial asthma or chronic obstructive
            pulmonary disease
  JOURNAL   Patent: EP 1394274-A 428 03-MAR-2004;
            Genox Research, Inc. (JP)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 5
AR366780
LOCUS       AR366780                1195 bp    DNA     linear   PAT 12-SEP-2003
DEFINITION  Sequence 1 from patent US 6329503.
ACCESSION   AR366780
VERSION     AR366780.1  GI:34599746
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE     Serpentine transmembrane antigens expressed in human cancers and
            uses thereof
  JOURNAL   Patent: US 6329503-A 1 11-DEC-2001;
            Agensys, Inc.; Santa Monica, CA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485
```

```
Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 6
AR405830
LOCUS       AR405830               1195 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 878 from patent US 6630305.
ACCESSION   AR405830
VERSION     AR405830.1  GI:40154667
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6630305-A 878 07-OCT-2003;
            Corixa Corporation; Seattle, WA;
            WOX;
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 7
AR564210
LOCUS       AR564210               1195 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 878 from patent US 6759515.
ACCESSION   AR564210
VERSION     AR564210.1  GI:53979261
```

```
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6759515-A 878 06-JUL-2004;
            Corixa Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

```
RESULT 8
AR589196
LOCUS       AR589196                1195 bp    DNA     linear   PAT 15-DEC-2004
DEFINITION  Sequence 878 from patent US 6800746.
ACCESSION   AR589196
VERSION     AR589196.1  GI:56636093
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A.W.,
            Hepler,W.T. and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: US 6800746-A 878 05-OCT-2004;
            Corixa Corporation; Seattle, WA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
```

Query Match 100.0%; Score 1017; DB 6; Length 1195;
Best Local Similarity 100.0%; Pred. No. 2.6e-231;
Matches 1017; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
```

```
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480

Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540

Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600

Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660

Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720

Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780

Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840

Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900

Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960

Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017

Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 9
AR654075
LOCUS       AR654075               1195 bp    DNA     linear   PAT 13-JUN-2005
DEFINITION  Sequence 1 from patent US 6887975.
ACCESSION   AR654075
VERSION     AR654075.1  GI:67584962
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Afar,D.E., Hubert,R.S., Leong,K., Raitano,A.B., Saffran,D.C. and
            Mitchell,S.C.
  TITLE     Peptides derived from STEAP1
  JOURNAL   Patent: US 6887975-A 1 03-MAY-2005;
            Agensys, Inc.; Santa Monica, CA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60

Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120

Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180

Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240

Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300

Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360

Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420

Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480

Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540

Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600

Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660

Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720

Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780

Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840

Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900

Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960

Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017

Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 10
AX201105
LOCUS       AX201105               1195 bp    DNA     linear   PAT 29-AUG-2001
DEFINITION  Sequence 735 from Patent WO0151633.
ACCESSION   AX201105
VERSION     AX201105.1  GI:15390890
KEYWORDS    .
```

```
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
            Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0151633-A 735 19-JUL-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 11
AX267904
LOCUS       AX267904                1195 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 878 from Patent WO0173032.
ACCESSION   AX267904
VERSION     AX267904.1  GI:16516522
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
            Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
            Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
            and Henderson,R.A.
  TITLE     Compositions and methods for the therapy and diagnosis of prostate
            cancer
  JOURNAL   Patent: WO 0173032-A 878 04-OCT-2001;
            CORIXA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
```

```
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 12
AX926483
LOCUS       AX926483               1195 bp    DNA     linear   PAT 19-DEC-2003
DEFINITION  Sequence 35 from Patent EP1355150.
ACCESSION   AX926483
VERSION     AX926483.1  GI:40246089
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wang,Y.
  TITLE     Panel of nucleic acid sequences for cancer diagnosis
  JOURNAL   Patent: EP 1355150-A 35 22-OCT-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082

RESULT 13
```

```
AX951736
LOCUS       AX951736               1195 bp    DNA     linear   PAT 08-JAN-2004
DEFINITION  Sequence 35 from Patent EP1367138.
ACCESSION   AX951736
VERSION     AX951736.1  GI:40782084
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Wang,Y.
  TITLE     Markers for breast cancer prognosis
  JOURNAL   Patent: EP 1367138-A 35 03-DEC-2003;
            Ortho Clinical Diagnostics Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082


RESULT 14
AX960014
LOCUS       AX960014               1195 bp    DNA     linear   PAT 14-JAN-2004
DEFINITION  Sequence 35 from Patent EP1349104.
ACCESSION   AX960014
VERSION     AX960014.1  GI:40880240
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jatkoe,T.
  TITLE     Method of selecting a portfolio of markers for use in a diagnostic
            application
  JOURNAL   Patent: EP 1349104-A 35 01-OCT-2003;
            Ortho-Clinical Diagnostics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1017;  DB 6;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
```

```
Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420

Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480

Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540

Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600

Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660

Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720

Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780

Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840

Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900

Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960

Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017

Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

```
RESULT 15
AF186249
LOCUS       AF186249                1195 bp    mRNA    linear   PRI 14-DEC-1999
DEFINITION  Homo sapiens six transmembrane epithelial antigen of prostate
            (STEAP1) mRNA, complete cds.
ACCESSION   AF186249
VERSION     AF186249.1  GI:6572947
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 1195)
  AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
            Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
            Jakobovits,A., Saffran,D.C. and Afar,D.E.
  TITLE     STEAP: a prostate-specific cell-surface antigen highly expressed in
            human prostate tumors
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (25), 14523-14528 (1999)
   PUBMED   10588738
REFERENCE   2  (bases 1 to 1195)
  AUTHORS   Hubert,R.S., Vivanco,I., Chen,E., Rastegar,S., Leong,K.,
            Mitchell,S.C., Madraswala,R., Zhou,Y., Kuo,J., Raitano,A.B.,
            Jakobovits,A., Saffran,D.C. and Afar,D.E.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-SEP-1999) UroGenesys Inc., 1701 Colorado Ave., Santa
            Monica, CA 90404, USA
FEATURES             Location/Qualifiers
     source          1. .1195
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="7"
                     /map="7p22.3"
     gene            1. .1195
                     /gene="STEAP1"
     CDS             66. .1085
                     /gene="STEAP1"
                     /note="cell surface protein"
                     /codon_start=1
                     /product="six transmembrane epithelial antigen of
                     prostate"
                     /protein_id="AAF17479.1"
                     /db_xref="GI:6572948"
                     /translation="MESRKDITNQEELWKMKPRRNLEEDDYLHKDTGETSMLKRPVLL
                     HLHQTAHADEFDCPSELQHTQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSH
                     QQYFYKIPILVINKVLPMVSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLT
                     RKQFGLLSFFFAVLHAIYSLSYPMRRSYRYKLLNWAYQQVQQNKEDAWIEHDVWRMEI
                     YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWNK
                     WIDIKQFVWYTPPTFMIAVFLPIVVLIFKSILFLPCLRKKILKIRHGWEDVTKINKTE
                     ICSQL"
ORIGIN
```

```
  Query Match             100.0%;  Score 1017;  DB 8;  Length 1195;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-231;
  Matches 1017;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60

Db         66 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 125

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120

Db        126 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 185

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180

Db        186 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 245

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240

Db        246 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 305

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300

Db        306 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 365

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360

Db        366 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 425

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420

Db        426 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 485

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480

Db        486 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 545

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540

Db        546 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 605

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600

Db        606 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 665
```

```
Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 725

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        726 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 785

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        786 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 845

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        846 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 905

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        906 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 965

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        966 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 1025

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1026 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1082
```

Search completed: December 5, 2005, 00:23:45
Job time : 5380.03 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 4, 2005, 20:37:26 ; Search time 4645.46 Seconds
(without alignments)
10242.778 Million cell updates/sec

Title: US-10-750-262-1_COPY_66_1082
Perfect score: 1017
Sequence: 1 atggaaagcagaaaagacat.....ctgagatatgttcccagttg 1017

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_htc:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1015.4	99.8	1050	10	AY403218	AY403218 Homo sapi
	2	904.6	88.9	1045	10	AY403219	AY403219 Pan trogl
	3	776	76.3	884	6	CA488012	CA488012 AGENCOURT
	4	738.6	72.6	1050	10	AY403220	AY403220 Mus muscu
	5	737	72.5	1211	4	AK010437	AK010437 Mus muscu
	6	692.8	68.1	881	2	BG565247	BG565247 602582917
	7	651	64.0	710	2	BE875216	BE875216 601488516
	8	639.2	62.9	827	8	CV983083	CV983083 UMC-bmix_
	9	623	61.3	961	2	BG762026	BG762026 602718984
	10	611.4	60.1	796	2	BG182296	BG182296 RST1161 A
c	11	605.4	59.5	720	6	CA446381	CA446381 UI-H-ED1-
	12	598	58.8	609	6	CD677954	CD677954 ho24h02.y
	13	598	58.8	697	8	DN997716	DN997716 TC115356
	14	597.8	58.8	920	2	BE881257	BE881257 601492338
	15	596	58.6	742	8	CX757709	CX757709 AGENCOURT
	16	592.6	58.3	773	5	BU602279	BU602279 AGENCOURT
	17	590	58.0	783	3	BI552907	BI552907 603197827
	18	589.6	58.0	825	8	CX753134	CX753134 AGENCOURT
	19	586.2	57.6	609	5	BX103101	BX103101 BX103101
c	20	584.4	57.5	788	7	CN153902	CN153902 941069 MA
	21	569.2	56.0	799	5	BU930271	BU930271 AGENCOURT
	22	557	54.8	1071	3	BM920324	BM920324 AGENCOURT
c	23	538	52.9	661	3	BM995067	BM995067 UI-H-ED0-
	24	536.6	52.8	1003	3	BI551229	BI551229 603194629
	25	522	51.3	684	2	BE439545	BE439545 HTM1-183F
	26	521.6	51.3	600	3	BI360480	BI360480 387409 MA
c	27	520	51.1	705	6	CB424830	CB424830 599432 MA
	28	511.2	50.3	636	6	CD690450	CD690450 EST6973 h
c	29	502	49.4	600	1	AI686139	AI686139 tt92e11.x
c	30	501.4	49.3	581	2	BG577403	BG577403 N112 SSH-
	31	494.4	48.6	891	2	BF965211	BF965211 602268114
	32	488.8	48.1	773	2	BG104394	BG104394 602311010
	33	485.2	47.7	779	5	BU929991	BU929991 AGENCOURT
	34	474.4	46.6	661	5	BX506262	BX506262 DKFZp686E
	35	472.6	46.5	1020	3	BM811413	BM811413 AGENCOURT
c	36	464.8	45.7	584	3	BM675259	BM675259 UI-E-EJ0-
	37	462	45.4	513	1	AA032221	AA032221 zf01e06.s
	38	461	45.3	705	5	BY755449	BY755449 BY755449
	39	460.4	45.3	581	3	BM714075	BM714075 UI-E-EJ0-
c	40	459.4	45.2	759	6	CA509933	CA509933 UI-R-FS0-
	41	455.4	44.8	468	6	CB119996	CB119996 K-EST0167
	42	442.8	43.5	791	2	BF573995	BF573995 602131824
c	43	438.8	43.1	729	3	BQ211210	BQ211210 UI-R-DY1-
c	44	433.2	42.6	654	7	CO594327	CO594327 DG2-93n7
c	45	429	42.2	696	3	BQ205543	BQ205543 UI-R-EP0-

ALIGNMENTS

RESULT 1
AY403218
LOCUS AY403218 1050 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens STEAP gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY403218
VERSION AY403218.1 GI:39759201
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1050)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1050)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES Location/Qualifiers
source 1. .1050
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
gene <1. .>1050
/gene="STEAP"
/locus_tag="HCM1484"
ORIGIN

Query Match 99.8%; Score 1015.4; DB 10; Length 1050;
Best Local Similarity 99.9%; Pred. No. 1.3e-259;
Matches 1016; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 90

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 150

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        151 CCTGTGCTTTTGCATTTGCAGCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 210

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 270

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 330

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 390

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 450

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 510

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 570

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 630

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 690

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 750

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 810

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 870

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 930

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 990

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1047
```

```
RESULT 2
AY403219
LOCUS       AY403219                1045 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Pan troglodytes STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403219
VERSION     AY403219.1  GI:39759202
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Pan.
REFERENCE   1  (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1045)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1045
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>1045
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

  Query Match             88.9%;  Score 904.6;  DB 10;  Length 1045;
  Best Local Similarity   89.2%;  Pred. No. 4.8e-230;
  Matches  907;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              |||||||      ||||||||||||||||||||||| ||||||
Db         26 ATGGAAANNNNNAAGACATCACAAACCAAGAAGAAATTTGGANNNNNNNNNNNNNNNNNN 85

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
                                     |||||||||||||||||||||||||||||||||||||
Db         86 NNNNNNNNNNNNNNNNNNNNNNNCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 145

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 205

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 265

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        266 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGGAGTAATTCACCCTTTAGCAACT 325

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 385

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 445

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        446 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 505

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 565

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATATCAACAGGTC 625

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||   |||||||||||||||||| ||||||||||||||||||||||||
Db        626 CAACAAAATAAAGANNNTGCCTGGATTGAGCATGACGTTTGGAGAATGGAGATTTATGTG 685

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        686 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGANNNNNNNNNNNNNN 745

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
                                                        ||||||||||||||||||
Db        746 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAGCAAGCTAGGAATTGTT 805

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTGCCTGGAATAAGTGGATAGATATA 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 TCCCTTCTACTGGGCACAATACACGCATTGATTTTGCCTGGAATAAGTGGATAGATATA 865

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 925

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 985

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        986 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATCTTCCCAGTTG 1042
```

RESULT 3
CA488012

```
LOCUS       CA488012                 884 bp    mRNA    linear   EST 14-NOV-2002
DEFINITION  AGENCOURT_10807821 MAPcL Homo sapiens cDNA clone IMAGE:6719746 5',
            mRNA sequence.
ACCESSION   CA488012
VERSION     CA488012.1  GI:24948800
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 884)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Kristi A. Egland, Ira Pastan
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM14278  row: c  column: 10
            High quality sequence stop: 758.
FEATURES             Location/Qualifiers
     source          1..884
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6719746"
                     /cell_line="ZR-75-1, MCF7, SK-BR-3, MDA-MB-231,
                     hTERT-HME1, LNCaP"
                     /lab_host="EMDH10B"
                     /clone_lib="MAPcL"
                     /note="Vector: pCMV-SPORT6; Site_1: EcoRV; Site_2: Not I;
                     Subtracted with brain, liver, lung, kidney and muscle.
                     Directionally cloned. Priming method: oligo-dT. Average
                     insert size: 1800 bp. Library amplification: 26,000 fold.
                     Kristi A. Egland, James J. Vincent, Robert Strausberg,
                     Bungkook Lee  & Ira Pastan:  Discovery of new breast
                     cancer genes encoding  membrane and secreted proteins.
                     Manuscript submitted."
ORIGIN

  Query Match             76.3%;  Score 776;  DB 6;  Length 884;
  Best Local Similarity   99.4%;  Pred. No. 9.9e-196;
  Matches  779;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         82 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 141

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 201

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 261

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 321

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        322 ATAGCATCTCTGACTTTTCTCTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 381

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        382 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 441

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 501

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 561

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 621

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        622 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGCATATCAACAGGTC 681

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        682 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 741

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        742 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 801

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |  |
Db        802 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAAATTGT 861

Qy        781 TCCC 784
              | ||
Db        862 TTCC 865
```

```
RESULT 4
AY403220
LOCUS       AY403220               1050 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus STEAP gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY403220
VERSION     AY403220.1  GI:39759203
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1050)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1. .1050
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>1050
                     /gene="STEAP"
                     /locus_tag="HCM1484"
ORIGIN

  Query Match             72.6%;  Score 738.6;  DB 10;  Length 1050;
  Best Local Similarity   82.9%;  Pred. No. 9.9e-186;
  Matches  843;  Conservative    0;  Mismatches  174;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||| | |||  | ||  | ||||||| |||| ||||||||||||||||||| | | ||
Db         31 ATGGAGATCAGTGACGATGTTACAAACCCAGAACAACTTTGGAAAATGAAGCCAAAGGGA 90

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||  | |||||  |||  ||| | |  ||||||| |||||||||| |||||||| ||||||
Db         91 AACCTGGAAGATGACAGTTACTCGACTAAGGACTCGGGAGAGACGAGCATGCTGAAAAGA 150

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              || | ||| | ||| ||||| ||  | | ||| |  ||||  |||||||||| || ||
Db        151 CCGGGGCTCTCGCACTTGCAGCACGCGGTCCACGTCGATGCCTTTGACTGCCCCTCCGAG 210

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              |||||||||| |||||| |||||||| | |||| ||||||| | ||| | ||||| ||
Db        211 CTTCAGCACACGCAGGAATTCTTTCCAAACTGGCGCTTGCCAGTGAAAGTCGCTGCCATC 270

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||| |||| |||||||| || ||||| |||||||||||| | ||  |||| |||| ||||
Db        271 ATATCATCCCTGACTTTCCTGTACACACTTCTGAGGGAAATCATCTACCCGTTAGTAACT 330

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              |||| | |||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        331 TCCCGTGAACAATATTTTTATAAAATTCCAATCCTGGTTATTAACAAAGTCTTGCCAATG 390

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              || |||| || ||||||||| |||| ||  ||||||| | | |||| ||| |||| ||
Db        391 GTCGCCATTACCCTCTTGGCACTGGTCTATTTGCCAGGAGAGTTAGCGGCAGTTGTACAG 450

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||  |||||||||||||| |||||||| ||||  ||||| ||||  |||||| |  |
Db        451 CTTCGCAATGGAACCAAGTACAAGAAGTTCCCACCCTGGTTAGATAGATGGATGCTGGCC 510

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              || |||||||||| || ||||| |||||||||||||| ||||| ||  |||| |||||
Db        511 AGGAAGCAGTTTGGTCTCCTCAGCTTCTTTTTTGCTGTGCTGCACGCTGTTTACAGTCTC 570

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              || |||||||||| |||||||||||||||| | || |||||||| ||  |||||||
Db        571 TCATACCCAATGAGGAGATCCTACAGATACAAGCTACTCAACTGGGCTTACAAACAGGTT 630

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              |||||||| ||||| ||||||||| | |||||||||| ||||||||||||||||||||
Db        631 CAACAAAACAAAGAGGATGCCTGGGTAGAGCATGATGTCTGGAGAATGGAGATTTATGTG 690

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              || ||||| ||||||||  |||| ||  ||||||| ||||||||||||||||||||||||
Db        691 TCCCTGGGGATTGTGGGGCTGGCCATCTTGGCTCTCTTGGCTGTGACATCTATTCCATCT 750

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||| |||||||| || ||||||||||||||||||||||||||||| ||||||||||
Db        751 GTGAGCGACTCTTTAACCTGGAGAGAATTTCACTATATTCAGAGCAAACTAGGAATTGTC 810

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              || ||||| ||||||||| ||||||| ||| |||||||||||||| ||| |||||  |
Db        811 TCTCTTCTTCTGGGCACAGTACACGCTTTGGTTTTTGCCTGGAATAAATGGGTAGATGTC 870

Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              |  |||||||||||||  |  ||||| |||||||||||||||||||||||||| | ||
Db        871 AGTCAATTTGTATGGTACATGCCTCCGACTTTTATGATAGCTGTTTTCCTTCCAACTCTT 930

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              |||||||||| ||||| |   || | |||||| ||  |||||||||||||||||||||||
Db        931 GTCCTGATATGTAAAATCGCCCTGTGCCTGCCCTGTCTGAGGAAGAAGATACTGAAGATT 990

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||  |||||||||||| |||| |||||||||  ||||||||    |||  ||||
Db        991 AGATGTGGTTGGGAAGATGTCAGCAAAATTAACAGGACTGAGATGGCCTCCAGGTTG 1047

RESULT 5
AK010437
LOCUS       AK010437               1211 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus ES cells cDNA, RIKEN full-length enriched library,
            clone:2410007B19 product:six transmembrane epithelial antigen of
            the prostate, full insert sequence.
ACCESSION   AK010437
VERSION     AK010437.1  GI:12845880
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
```

```
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1211)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
            Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,
            Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,
            Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
            Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES            Location/Qualifiers
     source         1. .1211
                    /organism="Mus musculus"
                    /mol_type="mRNA"
                    /strain="C57BL/6J"
                    /db_xref="FANTOM_DB:2410007B19"
                    /db_xref="taxon:10090"
                    /clone="2410007B19"
                    /cell_type="ES cells"
                    /clone_lib="RIKEN full-length enriched mouse cDNA library"
     CDS            98. .1117
                    /note="unnamed protein product; putative
                    six transmembrane epithelial antigen of the prostate
                    (MGD|MGI:1917608, GB|AK010437, evidence: BLASTN, 100%,
                    match=1211)"
                    /codon_start=1
                    /protein_id="BAB26938.1"
                    /db_xref="GI:12845881"
                    /translation="MEISDDVTNPEQLWKMKPKGNLEDDSYSTKDSGETSMLKRPGLS
                    HLQHAVHVDAFDCPSELQHTQEFFPNWRLPVKVAAIISSLTFLYTLLREIIYPLVTSR
                    EQYFYKIPILVINKVLPMVAITLLALVYLPGELAAVVQLRNGTKYKKFPPWLDRWMLA
                    KKQFGLLSFFFAVLHAVYSLSYPMRRSYRYKLLNWAYKQVQQNKEDAWVEHDVWRMEI
                    YVSLGIVGLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTVHALVFAWNK
                    WVDVSQFVWYMPPTFMIAVFLPTLVLICKIALCLPCLRKKILKIRCGWEDVSKINRTE
                    MASRL"
     polyA_signal   1186. .1191
                    /note="putative"
     polyA_site     1211
                    /note="putative"
ORIGIN

  Query Match             72.5%;  Score 737;  DB 4;  Length 1211;
  Best Local Similarity   82.8%;  Pred. No. 2.7e-185;
  Matches  842;  Conservative    0;  Mismatches  175;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||| | |||  | ||  | |||||||| |||| ||||||||||||||||||| | | ||
Db         98 ATGGAGATCAGTGACGATGTTACAAACCCAGAACAACTTTGGAAAATGAAGCCAAAGGGA 157

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||  | ||||| |||  ||| | |  ||||||| |||||||||| |||||||| ||||||
Db        158 AACCTGGAAGATGACAGTTACTCGACTAAGGACTCGGGAGAGACGAGCATGCTGAAAAGA 217

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              || | ||| | ||| ||||| ||  | | ||| |  ||||  |||||||||||| || ||
Db        218 CCGGGGCTCTCGCACTTGCAGCACGCGGTCCACGTCGATGCCTTTGACTGCCCCTCCGAG 277

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              |||||||||||| |||||| |||||||| | |||| ||||||| | ||| | ||||| ||
Db        278 CTTCAGCACACGCAGGAATTCTTTCCAAACTGGCGCTTGCCAGTGAAAGTCGCTGCCATC 337

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||| |||| |||||||| || ||||| |||||||||||| | ||  |||| |||| ||||
Db        338 ATATCATCCCTGACTTTCCTGTACACACTTCTGAGGGAAATCATCTACCCGTTAGTAACT 397

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              |||| | |||||||||||||||||||||||||||||| || ||||||||||||||||||
Db        398 TCCCGTGAACAATATTTTTATAAAATTCCAATCCTGGTTATTAACAAAGTCTTGCCAATG 457

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||  |||| || ||||||||| |||| ||  ||||||| | | |||| ||| |||| ||
Db        458 GTCGCCATTACCCTCTTGGCACTGGTCTATTTGCCAGGAGAGTTAGCGGCAGTTGTACAG 517

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||  |||||||||||||| |||||||| |||| |||||  |||| |||||||  | |
Db        518 CTTCGCAATGGAACCAAGTACAAGAAGTTCCCACCCTGGTTAGATAGATGGATGCTGGCC 577

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              |  |||||||||| || ||||| |||||||||||||| ||||| ||  |||| |||||
Db        578 AAGAAGCAGTTTGGTCTCCTCAGCTTCTTTTTTGCTGTGCTGCACGCTGTTTACAGTCTC 637

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              || |||||||||||| |||||||||||||||| | || |||||||| ||  |||||||
Db        638 TCATACCCAATGAGGAGATCCTACAGATACAAGCTACTCAACTGGGCTTACAAACAGGTT 697

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              |||||||| ||||| |||||||| | |||||||||||| ||||||||||||||||||||
Db        698 CAACAAAACAAAGAGGATGCCTGGGTAGAGCATGATGTCTGGAGAATGGAGATTTATGTG 757

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              || ||||| |||||||  |||| ||  ||||||| ||||||||||||||||||||||||
Db        758 TCCCTGGGGATTGTGGGGCTGGCCATCTTGGCTCTCTTGGCTGTGACATCTATTCCATCT 817

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTT 780
              ||||| |||||||| || ||||||||||||||||||||||||||| ||||||||||
Db        818 GTGAGCGACTCTTTAACCTGGAGAGAATTTCACTATATTCAGAGCAAACTAGGAATTGTC 877

Qy        781 TCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATA 840
              || ||||| |||||||| ||||||| ||| |||||||||||||| ||| ||||| |
Db        878 TCTCTTCTTCTGGGCACAGTACACGCTTTGGTTTTTGCCTGGAATAAATGGGTAGATGTC 937
```

```
Qy        841 AAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTT 900
              |  ||||||||||||||| |  ||||| |||||||||||||||||||||||||| | ||
Db        938 AGTCAATTTGTATGGTACATGCCTCCGACTTTTATGATAGCTGTTTTCCTTCCAACTCTT 997

Qy        901 GTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGATACTGAAGATT 960
              |||||||||| ||||| |   || | |||||| ||  |||||||||||||||||||||||
Db        998 GTCCTGATATGTAAAATCGCCCTGTGCCTGCCCTGTCTGAGGAAGAAGATACTGAAGATT 1057

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTCCCAGTTG 1017
              |||  |||||||||||| |||| ||||||||||  ||||||||    |||  ||||
Db       1058 AGATGTGGTTGGGAAGATGTCAGCAAAATTAACAGGACTGAGATGGCCTCCAGGTTG 1114


RESULT 6
BG565247
LOCUS       BG565247                881 bp    mRNA    linear   EST 10-APR-2001
DEFINITION  602582917F1 NIH_MGC_76 Homo sapiens cDNA clone IMAGE:4710436 5',
            mRNA sequence.
ACCESSION   BG565247
VERSION     BG565247.1  GI:13572900
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 881)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1549  row: b  column: 05
            High quality sequence stop: 704.
FEATURES             Location/Qualifiers
     source          1. .881
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4710436"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_76"
                     /note="Organ: liver; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.85
                     kb (range 1.0-4.0 kb). 15/15 colonies contained  inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             68.1%;  Score 692.8;  DB 2;  Length 881;
  Best Local Similarity   93.6%;  Pred. No. 1.6e-173;
  Matches  777;  Conservative    0;  Mismatches   47;  Indels    6;  Gaps    5;

Qy        186 GCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGC 245
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGC 60

Qy        246 ATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCA 305
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCA 120

Qy        306 TCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTC 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTC 180

Qy        366 CATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCA 425
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCA 240

Qy        426 TAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAA 485
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TAATGGAACCAAGTATAAGAAGTTTCCACAGTGGTTGGATAAGTGGATGTTAACAAGAAA 300

Qy        486 GCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTA 545
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTA 360

Qy        546 CCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACA 605
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACA 420

Qy        606 AAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT 665
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAATAAAGAAGATGCCTGGATTGAGCATGATGTCTGGAGAATGGAGATTTATGTGTCTCT 480

Qy        666 GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAG 725
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        481 GGGAATTGTGGGATTGG-AATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAG 539

Qy        726 TGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCT 785
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 TGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGGAAGCTAGGAATAGTTTCCCT 599

Qy        786 TCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGG--ATAGATATAAAA 843
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 TCTACTGGGCACAATACACGCATTGATTTTGGCCTGGAATAAGTGGGATAGATCATAAAC 659

Qy        844 CAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTC 903
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        660 ACAATTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTCCTTCCAATTGTAGTCC 719

Qy        904 CTGATATTT-AAAAGCATACTATT-CCTGCCATGCTTGAGGAAGAAGATACT-GAAGATT 960
              ||||||||| ||| |||||||||| | |||||||||||| | |||||||||| || ||||
Db        720 CTGATATTTCAAACGCATACTATTACTTGCCATGCTTGAAGCAGAAGATACTGGACGATT 779

Qy        961 AGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTC 1010
              |||| ||||||||||||      |    ||      |||||||||| ||| |
Db        780 AGACTTGGTTGGGAAGAACGTCCACCAAAATCAAAAACTGAGATTTGTCC 829


RESULT 7
BE875216
LOCUS       BE875216                710 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601488516F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3890930 5',
            mRNA sequence.
ACCESSION   BE875216
VERSION     BE875216.1  GI:10323992
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 710)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
```

found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9674 row: p column: 03
High quality sequence stop: 701.

```
FEATURES             Location/Qualifiers
     source          1. .710
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3890930"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.1 kb. Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             64.0%;  Score 651;  DB 2;  Length 710;
  Best Local Similarity   99.0%;  Pred. No. 2.2e-162;
  Matches  676;  Conservative    0;  Mismatches    5;  Indels    2;  Gaps    2;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         22 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAC-TTGGAAAATGAAGCCTAGGAGA 80

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         81 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAGAGA 140

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 200

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 260

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 320

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 380

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 440

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 500

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 560

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 620

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGG-AGATTTATGT 659
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        621 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGCAGATTTATGT 680

Qy        660 GTCTCTGGGAATTGTGGGATTGG 682
              |||||||||||| ||||| | |
Db        681 GTCTCTGGGAATCGTGGGGATTG 703
```

RESULT 8

```
CV983083
LOCUS       CV983083                827 bp    mRNA    linear   EST 30-NOV-2004
DEFINITION  UMC-bmix_0B02-007-e08 Conceptus-Corpus Luteum (mixed) bmix Bos
            taurus cDNA 3', mRNA sequence.
ACCESSION   CV983083
VERSION     CV983083.1  GI:56143804
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
            Pecora; Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 827)
  AUTHORS   Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
            Roberts,R.M., Smith,M.F. and Youngquist,R.S.
  TITLE     USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
            Reproduction
  JOURNAL   Unpublished (2002)
COMMENT     Contact: DNA Core Facility (Bovine Project)
            Animal Science - RS Prather
            University of Missouri-Columbia
            M616 Medical Sciences Bldg., Columbia, MO 65212, USA
            Tel: (573)882-0428
            Fax: (573)884-5552
            Email: bovine@rnet.missouri.edu
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .827
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /dev_stage="Conceptus-Corpus Luteum(mixed)"
                     /clone_lib="bmix"
                     /note="Vector: pSport1; Funding: The production of ESTs
                     submitted in this project was funded by USDA Grant
                     MRI-2002-03476 entitled 'Bovine ESTs: Focus on Female
                     Reproduction' to RS Prather(Primary Investigator), E
                     Antoniou, HA Garverick, JA Green, MC Lucy, RM Roberts, MF
                     Smith and RS Youngquist. Genetic Source: Heifers for the
                     project were purchased from Circle A Ranch, Iberia, MO
                     (http://www.circlearanch.com/home.html). These heifers,
                     while not registered have known Angus pedigrees going back
                     at least 4 generations. Samples collected: The samples
                     consisted of the following: germinal vesicle-stage
                     oocytes; in vitro derived embryos (2-cell, morula,
                     blastocyst and nuclear transfer blastocyst); in vivo
                     blastocysts and conceptuses (days 8, 14, 16 and 18);
                     corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
                     follicles (days 0, non-recruited, recruited, early
                     selected and preovulatory); oviduct (days 0, 3 and 5);
                     endometrium (days 5, 8, 14, 16, 18 and 35); and
                     placenta/embryo from day 35 conceptuses. Expanded
                     descriptions of how the tissues were collected can be
                     found at the following URL:
                     http://genome.rnet.missouri.edu/Bovine/Methods.html.
                     Library construction (Standard Protocol): All procedures
                     have been described in detail elsewhere (Soares et al.,
                     1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
                     cellular RNA from each sample was isolated by using
                     STAT-60 reagent (Tel-Test, Friendswood, TX) and the
                     poly(A)+ RNA was obtained by two rounds of purification
                     with the Oligotex mRNA isolation kit (Qiagen) according to
                     the manufacturer's instructions. The libraries were
                     constructed essentially as described by the manufacturer's
                     instructions provided with the SuperScript Plasmid System
                     (Invitrogen, cat. no. 18248-013). Briefly, 1mcg of
                     poly(A)+ RNA was annealed at c37 degrees with 10mcg of
                     NotI-tag-dT18 oligonucleotide (GCTGCTCGCGGCCGC-tag-T18)
                     and reverse transcribed at c37 degrees with SuperScript II
                     (Invitrogen) reverse transcriptase (Jiang et al., 2001).
                     The 'tag' represents a tissue/stage-specific ten-base
                     sequence identifier
                     (http://genome.uiowa.edu/pubsoft/software.html) present in
```

the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs were ligated to SalI adapters (Invitrogen-Life Technologies) and digested with NotI. The cDNAs were size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and SalI sites of the pCMV-SPORT6 vector (Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing. Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: bovine@rnet.missouri.edu. Citations: Bonaldo MF, Lennon G, Soares MB,. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.
TAG_TISSUE=Conceptus-Corpus Luteum (mixed)
TAG_SEQ=Not found"

ORIGIN

Query Match 62.9%; Score 639.2; DB 8; Length 827;
Best Local Similarity 90.2%; Pred. No. 3.2e-159;
Matches 683; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 ATGGAGAGCAGACAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 130

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||| |||||||||| ||||||||| |||| ||| | | ||||| | ||||||| ||||||
Db        131 AATCTAGAAGAAGATGATTATTTGAATAAAGACTCAGAAGAGATCGGCATGCTGAAAAGA 190

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              | |||||||||||| |||||||||||| |||||  |||||||||||| |||||  ||||
Db        191 CATGTGCTTTTGCACTTGCACCAAACAACCCATTTTGATGAATTTGATTGCCCCCCAGAG 250

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              |||||||| | |||| |||||||||||| |||||| ||||||||||||||||| ||||||
Db        251 CTTCAGCAAAAACAGAAACTCTTTCCAAAGTGGCGCTTGCCAATTAAAATAGCCGCTATT 310

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
               || |||||||||||||||| ||||||||| |||||||| |||||||||||||| |  |||
Db        311 GTATCATCTCTGACTTTTCTCTACACTCTTGTGAGGGAAATAATTCACCCTTTTGTGACT 370

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        371 TCCCATCAACAGTATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 430

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              |||||||||| ||||||||| ||||||| |||||||||||||||||||| |||| ||
Db        431 GTTTCCATCACCCTCTTGGCACTGGTTTATTTGCCAGGTGTGATAGCAGCAGTTGTGCAG 490

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              |||||||||||||| |||||||||| ||||| || |||||||||| ||||||| |||||
Db        491 CTTCATAATGGAACTAAGTATAAGAAATTTCCGCACTGGTTGGATAGGTGGATGGTAACA 550

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              |||||||||||||| |||||||||||||||||||||||||| |||||||||| ||| |
Db        551 AGAAAGCAGTTTGGTCTTCTCAGTTTCTTTTTTGCTGTACTACATGCAATTTACAGTTTA 610

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              || || || |||||||||||||||||| | |||||| |||||||||||||||||||||
Db        611 TCCTATCCGATGAGGCGATCCTACAGATATAGGTTGCTGAACTGGGCATATCAACAGGTC 670

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTG 660
              |||||||||| ||| |||||||||||| ||||||||||||||||||||| ||||||||
Db        671 CAACAAAATAACGAANATGCCTGGATTGAACATGATGTTTGGAGAATGGAAATTTATGTA 730

Qy        661 TCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCT 720
              || |||||||| |||| | | |||||||| ||||| ||||||||||||||||||||||||
Db        731 TCACTGGGAATCGTGGCACTTGCAATACTAGCTCTATTGGCTGTGACATCTATTCCATCT 790

Qy        721 GTGAGTGACTCTTTGACATGGAGAGAATTTCACTATA 757
              |||||||| ||| ||||||||||||||||||||||||
Db        791 GTGAGTGATTCTCTGACATGGAGAGAATTTCACTATA 827
```

RESULT 9
BG762026

```
LOCUS       BG762026                961 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602718984F1 NIH_MGC_49 Homo sapiens cDNA clone IMAGE:4858820 5',
            mRNA sequence.
ACCESSION   BG762026
VERSION     BG762026.1  GI:14072679
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 961)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1713  row: h  column: 21
            High quality sequence stop: 750.
FEATURES             Location/Qualifiers
     source          1. .961
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4858820"
                     /tissue_type="melanotic melanoma, high MDR (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_49"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
```

using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"
ORIGIN

Query Match 61.3%; Score 623; DB 2; Length 961;
Best Local Similarity 93.1%; Pred. No. 7e-155;
Matches 710; Conservative 0; Mismatches 40; Indels 13; Gaps 5;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        122 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAATTTGGAAAATGAAGCCTAGGAGA 181

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AATTTAGAAGACAACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 241

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        242 CCTGTGCTTTTGCATTTGCAGCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 301

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CTTCAGCACGCACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTGTT 361

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 ATGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 421

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 481

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        482 GTTTCCATCACTCTCTTGGCATTGGTTTACCTACCAGGTGTGATAGCAGCAATTGTCCAA 541

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 GTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 601

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              |||||||||||||||||||||||||  |||||||||||||||||||||||||| ||||
Db        602 AGAAAGCAGTTTGGGCTTCTCAGTTT-GGTTTTGCTGTACTGCATGCAATTTATACTCTG 660

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TCTTACGCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 720

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAAT--GGAGATTTATG 658
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||  |    || |||
Db        721 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTCGGAGAATGCGCCACTTCATG 780

Qy        659 TGTCTCTGGGAATTGTGGGATTGGC-------AATACTGGCTCTGTTGGC--TGTGACAT 709
              |||| | ||| | | || |   | |         |   ||||||||||||    ||||||
Db        781 TGTCCCCGGGGACTTTGTGGCGGACGGGGCAACACTTGGGCTCTGTTGGCCTGTTGACAT 840

Qy        710 CTATTCCATCTGTGA-GTGACTCTTTGACATGGAGAGAATTTC 751
              ||||||||||||||| ||||| ||||||| ||| ||||||| |
Db        841 CTATTCCATCTGTGACGTGACCCTTTGACCTGGCGAGAATTCC 883
```

RESULT 10
BG182296
LOCUS BG182296 796 bp mRNA linear EST 21-APR-2001
DEFINITION RST1161 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG182296
VERSION BG182296.1 GI:13703983
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 796)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 505.
FEATURES Location/Qualifiers
source 1. .796
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN

Query Match 60.1%; Score 611.4; DB 2; Length 796;
Best Local Similarity 97.2%; Pred. No. 8.3e-152;
Matches 632; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        147 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAAATTTGGAAAATGAAGCCTAGGAGA 206

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              |||||||||||  ||||||||||||||| ||||||||||||||||||||||||||||||
Db        207 AATTTAGAAGACAACGATTATTTGCATGAGGACACGGGAGAGACCAGCATGCTAAAAAGA 266

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        267 CCTGTGCTTTTGCATTTGCAGCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 326

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||| ||
Db        327 CTTCAGCACGCACAGGAACTCTTACCACAGTGGCACTTGCCAATTAAAATAGCTGCTGTT 386

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 ATGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 446

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 506

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        507 GTTTCCATCACTCTCTTGGCATTGGTTTACCTACCAGGTGTGATAGCAGCAATTGTCCAA 566

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 GTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 626

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              |||||||||||||||||||||||||  |||||||||||||||||||||||||| ||||
Db        627 AGAAAGCAGTTTGGGCTTCTCAGTTTGTTTTTTGCTGTACTGCATGNCATTTATACTCTG 686
```

```
Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 TCTTACGCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 746

Qy        601 CAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGA 650
              |||| |||||||||||||||||||||||||||||||||||| ||||||
Db        747 CAAC-AAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAAAATGGA 795


RESULT 11
CA446381/c
LOCUS       CA446381                720 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-ED1-axr-o-23-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
            UI-H-ED1-axr-o-23-0-UI 3', mRNA sequence.
ACCESSION   CA446381
VERSION     CA446381.1  GI:24810801
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 720)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .720
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-ED1-axr-o-23-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_ED1"
                     /note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_ED1 is a normalized cDNA library
                     containing the following tissue(s): Chondrosarcoma cell
                     line CS5. The library was constructed according to
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. First strand cDNA synthesis was primed with an
                     oligo-dT primer containing a Not I site. Double stranded
                     cDNA was ligated to an EcoR I adaptor, digested with Not
                     I, and cloned directionally into pT7T3-Pac vector. The
                     oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is GCTCAAGGCT.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-ED1
                     TAG_SEQ=CGTCAAGGCT"
ORIGIN

  Query Match             59.5%;  Score 605.4;  DB 6;  Length 720;
  Best Local Similarity   99.8%;  Pred. No. 3.3e-150;
  Matches  606;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        411 AATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTG 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        720 AATTGTCCAACTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTG 661

Qy        471 GATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAAT 530
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        660 GATGTTAACAAGAAAGCAGTCTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAAT 601

Qy        531 TTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATA 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        600 TTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATA 541

Qy        591 TCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGA 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 TCAACAGGTCCAACAAAATAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGA 481

Qy        651 GATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATC 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 GATTTATGTGTCTCTGGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATC 421

Qy        711 TATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCT 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TATTCCATCTGTGAGTGACTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCT 361

Qy        771 AGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTG 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AGGAATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTG 301

Qy        831 GATAGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GATAGATATAAAACAATTTGTATGGTATACACCTCCAACTTTTATGATAGCTGTTTTCCT 241

Qy        891 TCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAT 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TCCAATTGTTGTCCTGATATTTAAAAGCATACTATTCCTGCCATGCTTGAGGAAGAAGAT 181

Qy        951 ACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTC 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 ACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACTGAGATATGTTC 121

Qy       1011 CCAGTTG 1017
              |||||||
Db        120 CCAGTTG 114


RESULT 12
CD677954
LOCUS       CD677954                609 bp    mRNA    linear   EST 24-JUN-2003
DEFINITION  ho24h02.y1 Human Trabecular meshwork cDNA: hohphq Homo sapiens cDNA
            clone ho24h02 5', mRNA sequence.
ACCESSION   CD677954
VERSION     CD677954.1  GI:32179685
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 609)
  AUTHORS   Tomarev,S.I., Wistow,G., Raymond,V., Dubois,S. and Malyukova,I.
  TITLE     Gene expression profile of the human trabecular meshwork: NEIBank
            sequence tag analysis
  JOURNAL   Invest. Ophthalmol. Vis. Sci. 44 (6), 2588-2596 (2003)
   PUBMED   12766061
COMMENT     Contact: Wistow G
            Section on Molecular Structure and Function
            National Eye Institute
            6/331, NIH, Bethesda, MD 20892-2740, USA
            Tel: 301 402 3452
            Fax: 301 496 0078
            Email: graeme@helix.nih.gov
            Plate: 24  row: h  column: 02
            Seq primer: M13RP1 reverse primer (ABI).
FEATURES             Location/Qualifiers
     source          1. .609
                     /organism="Homo sapiens"
```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="ho24h02"
/tissue_type="Trabecular meshwork"
/dev_stage="Adult"
/lab_host="EMDH10B"
/clone_lib="Human Trabecular meshwork cDNA: hohphq"
/note="Organ: Eye; Vector: pSPORT1; The cDNA, directionally cloned in the pSPORT1 vector (Life Technologies, Rockville, MD), was constructed at Bioserve Biotechnology (Laurel, MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (http://www.lifetech.com/). Sublibraries (designated ho, hp, and hq) were made from the first three 35-uL fractions of cDNA from a Sephacryl S-500 HR resin column. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center(NISC)."

ORIGIN

Query Match 58.8%; Score 598; DB 6; Length 609;
Best Local Similarity 99.8%; Pred. No. 3e-148;
Matches 609; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
Qy        189 CACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATC 248
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db          1 CACACAGGAACTCTTTCCA-AGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATC 59

Qy        249 TCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCA 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 TCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCA 119

Qy        309 ACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCAT 368
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 ACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCAT 179

Qy        369 CACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAA 428
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 CACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAA 239

Qy        429 TGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCA 488
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        240 TGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCA 299

Qy        489 GTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCC 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        300 GTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCC 359

Qy        549 AATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAA 608
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 AATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAA 419

Qy        609 TAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGG 668
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 TAAAGAAGATGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGG 479

Qy        669 AATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGA 728
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 AATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGA 539

Qy        729 CTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCT 788
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 CTCTTTGACATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCT 599

Qy        789 ACTGGGCACA 798
              ||||||||||
Db        600 ACTGGGCACA 609
```

RESULT 13
DN997716
LOCUS DN997716 697 bp mRNA linear EST 17-MAY-2005
DEFINITION TC115356 Human breast cancer tissue, large insert, pCMV expression library Homo sapiens cDNA clone TC115356 5' similar to Homo sapiens six transmembrane epithelial antigen of the prostate 1 (STEAP1), mRNA sequence.
ACCESSION DN997716
VERSION DN997716.1 GI:66257543
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 697)
AUTHORS Birkett,C., Cho,J., Gau,Y., Hamer,R., Kelly,S., Kovacs,K., Liu,L., Liu,X., Porter,J., Sachs,A., Shu,Y., Sun,Z., Wong,J., Wu,M., Zhang,X., Jay,G. and He,W.
TITLE High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
JOURNAL Unpublished (2005)
COMMENT Contact: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. (www.origene.com)
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length cloning project at OriGene Technologies, Inc.
Please contact OriGene for access.
OriGene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
Seq primer: pCMV6 5prime forward vector primer, OriGene Technologies Inc.
FEATURES Location/Qualifiers
source 1. .697
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC115356"
/tissue_type="Breast cancer"
/clone_lib="Human breast cancer tissue, large insert, pCMV expression library"
/note="Organ: Mammary gland (cancer tissue); Vector: pCMV6-XL5; Site_1: EcoR1; Site_2: Xho1/Sal1 compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"

ORIGIN

Query Match 58.8%; Score 598; DB 8; Length 697;
Best Local Similarity 100.0%; Pred. No. 3.1e-148;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 159

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 219

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 279

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 339
```

```
Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 399

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 459

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 519

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 579

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 639

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGG 598
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGG 697
```

RESULT 14
BE881257

```
LOCUS       BE881257                920 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601492338F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3894657 5',
            mRNA sequence.
ACCESSION   BE881257
VERSION     BE881257.1  GI:10330033
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 920)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9684  row: k  column: 10
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1. .920
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3894657"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN
```

```
  Query Match             58.8%;  Score 597.8;  DB 2;  Length 920;
  Best Local Similarity   93.4%;  Pred. No. 3.7e-148;
  Matches  724;  Conservative    0;  Mismatches   37;  Indels   14;  Gaps    9;

Qy        138 GCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGA 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGA 60

Qy        198 ACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATTATAGCATCTCTGACTTT 120

Qy        258 TCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACTTCCCATCAACAATATTT 180

Qy        318 TTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATGGTTTCCATCACTCTCTT 240

Qy        378 GGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACTTCATAATGGAACCAA 437
              |||| |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        241 GGCA-TGGTTTACCTGCCAGGTGTGATAGCAGCAA-TGTCCAACTTCATAATGGAACCAA 298

Qy        438 GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCT 497
              |||||||||||||||| |||||||||||||||||||||||||||||| |||||||
Db        299 GTATAAGAAGTTTCCACA-TGGTTGGATAAGTGGATGTTAACAAGAAAGCAG-TTGGGCT 356

Qy        498 TCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCG 557
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 TCTCAGTTTC-TTTTTGCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCG 415

Qy        558 ATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGA 617
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        416 ATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTCCAACAAAATAAAGAAGA 475

Qy        618 TGCCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGG 677
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        476 TGCCTGGATTGAGCATGATG-TTGGAGAATGGAGATTTATGTGTCTCTGGGAATTGTGGG 534

Qy        678 ATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGAC 737
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        535 ATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGAC 594

Qy        738 ATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAATTGTTTCCCTTCTACTGGGCAC 797
              |||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||||||
Db        595 ATGGAGAGAATTTCACTATATTCAGAGCAAGCTAGGAA-TGTGTCCCTTCTACTGGGCAC 653

Qy        798 AATACACGCATTGATTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTGTATGGTA 857
              |||||||||||||||        | ||||||||||||||||    ||  |   |||||
Db        654 AATACACGCATTGATTT---GGCTGGATAAGTGGATAGATATA----AACATTGTTGGTA 706

Qy        858 TACACCTCCAACTTTTATGATAGCTGTTTTCCTTCCAATTGTTGTCCTGATATTT 912
              ||||||||||  || |   |  | |   |||  |    |||| |    ||| |
Db        707 TACACCTCCACTTTATGATAGTGTTTCCTTCAATGTGTCTGTTATTAAAGTATAT 761
```

RESULT 15
CX757709

```
LOCUS       CX757709                742 bp    mRNA    linear   EST 24-JAN-2005
DEFINITION  AGENCOURT_41384224 NIH_MGC_278 Homo sapiens cDNA clone
            IMAGE:7772991 3', mRNA sequence.
ACCESSION   CX757709
VERSION     CX757709.1  GI:58054365
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
```

```
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Meri Firpo
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15916  row: h  column: 13
            High quality sequence start: 6
            High quality sequence stop: 726.
FEATURES             Location/Qualifiers
     source          1. .742
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:7772991"
                     /tissue_type="pluripotent cell line derived from
                     blastocyst inner cell mass"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_278"
                     /note="Organ: Blastocyst; Vector: pExpress-1; Site_1:
                     EcoRV; Site_2: NotI; RNA obtained from pluripotent cell
                     line derived from blastocyst inner cell mass (cell line
                     HSF-1.14, NIH Registry designation UC01. Positive for OCT4
                     expression by rtPCR, positive for SSEA-3, SSEA-4,
                     Tra-1-81, Tra-1-60 by immunofluorescence. Negative for
                     SSEA-1 by immunofluorescence. Passage 35. This line is a
                     subclone of the parental line; the parental line was
                     subcloned to remove aneuploid cells). cDNA was primed
                     using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.25
                     kb resulted in an average insert size of 1.9 kb. This
                     primary library is non-normalized (normalized primary
                     library is NIH_MGC_279) and was constructed by Express
                     Genomics (Frederick, MD). Note: this is a Mammalian Gene
                     Collection library."
ORIGIN

  Query Match             58.6%;  Score 596;  DB 8;  Length 742;
  Best Local Similarity   97.6%;  Pred. No. 1.1e-147;
  Matches  605;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 ATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGGAGA 60
              |||||||||||||||| |||||||||||||| |||||||||||||||||||||||||||
Db        123 ATGGAAAGCAGAAAAGACGTCACAAACCAAGAAGAAATTTGGAAAATGAAGCCTAGGAGA 182

Qy         61 AATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 120
              |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        183 AATTTAGAAGACAACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGA 242

Qy        121 CCTGTGCTTTTGCATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 180
              |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        243 CCTGTGCTTTTGCATTTGCAGCGAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAA 302

Qy        181 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTATT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        303 CTTCAGCACACACAGGAACTCTTTCCACAGTGGCACTTGCCAATTAAAATAGCTGCTGTT 362

Qy        241 ATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 300
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ATGGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATTCACCCTTTAGCAACT 422

Qy        301 TCCCATCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAATG 360
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        423 TCCCGTCAACAATATTTTTATAAAATTCCAATCCTGGTCATCAACAAAGTCTTGCCAGTG 482

Qy        361 GTTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAA 420
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        483 GTTTCCATCACTCTCTTGGCATTGGTTTACCTACCAGGTGTGATAGCAGCAATTGTCCAA 542

Qy        421 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        543 CTTCATAATGGAACCAAGTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACA 602

Qy        481 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATAGTCTG 540
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db        603 AGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTTGCTGTACTGCATGCAATTTATACTCTG 662

Qy        541 TCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 600
              |||||| |||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        663 TCTTACGCAATGATGCGATCCTACAGATACAAGTTGCTAAACTGGGCATATCAACAGGTC 722

Qy        601 CAACAAAATAAAGAAGATGC 620
              |||||||| ||||||||||
Db        723 CAACAAAATGAAGAAGATGC 742


Search completed: December  5, 2005, 03:12:15
Job time : 4648.46 secs
```